

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 16, 2005, 21:58:20 ; Search time 11350 Seconds
(without alignments)
4653.408 Million cell updates/sec

Title: US-09-833-222a-10
Perfect score: 5726
Sequence: 1 MAVALGTRRRDRVKLWADTF.....MPMNTVPVVLGGNIRVVAL 1090

Scoring table:

BLOSUM62	Xgapop 10.0	Xgapext 0.5
Ygapop 10.0	Ygapext 0.5	
Zgapop 6.0	Zgapext 7.0	
Delop 6.0	Delext 7.0	

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=GenEmbl -OPMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LQOPEL=0 -LQOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

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4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

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11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5399.5	94.3	4604	9 AF516695	AF516695 Homo sapi
2	5386.5	94.1	5073	6 BD248445	BD248445 Alpha-2/d
3	5373.5	93.8	5359	9 HSM805741	BX537437 Homo sapi
4	5342.5	93.3	3339	6 AX098927	AX098927 Sequence

5	5342.5	93.3	3339	6	AX099347	Sequence
6	5276	92.1	3209	6	AX098926	Sequence
7	5276	92.1	3209	6	AX099346	Sequence
8	5244.5	91.6	5001	6	BD248454	Alpha-2/d
9	5239.5	91.5	5960	6	HSM805740	Homo sapi
10	5214.5	91.1	5712	6	BD248455	Alpha-2/d
11	5148	89.9	3201	6	AX098925	Sequence
12	5148	89.9	3201	6	AX099345	Sequence
13	3808	66.5	4125	6	AX302028	Sequence
14	3423.5	59.8	3710	10	MMU010949	Sequence
15	3421.5	59.8	3276	10	AF486278	Rattus no
16	3421.5	59.8	3544	9	HSJ272268	Homo sapi
17	3416.5	59.7	3276	6	AR454329	Sequence
18	3416.5	59.7	3276	6	AX427033	Sequence
19	3416.5	59.7	3653	9	AF516696	Homo sapi
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21	3416.5	59.7	3690	6	AX427031	Sequence
22	3410.5	59.6	3770	6	BD248444	Alpha-2/d
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24	3410.5	59.6	3770	6	AX099316	Sequence
25	3400.5	59.4	3213	6	AX098884	Sequence
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28	3326.5	58.1	3114	6	AX099303	Sequence
29	3297	57.6	3464	9	HSJ272213	Homo sapi
30	3278.5	57.3	3057	6	AX098882	Sequence
31	3278.5	57.3	3057	6	AX099302	Sequence
32	3222	56.3	3598	6	BD248481	Alpha-2/d
33	2026.5	35.4	2008	6	BD248480	Alpha-2/d
34	1868.5	32.6	2944	9	HSM801956	Homo sapi
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36	1792.5	31.3	1050	6	AX099310	Sequence
37	1695	29.6	969	6	AX098889	Sequence
38	1695	29.6	969	6	AX099309	Sequence
39	1598	27.9	912	6	AX098888	Sequence
40	1598	27.9	912	6	AX099308	Sequence
41	1552	27.1	6395	3	AY069830	Drosophil
42	1497.5	26.2	5862	6	AX155081	Sequence
43	1410	24.6	6519	6	CQ602907	Sequence
44	1362.5	23.8	856	6	AX552194	Sequence
45	1336.5	23.3	3414	6	CQ585735	Sequence

ALIGNMENTS

RESULT 1	AF516695	4604 bp	mRNA	linear	PRI 10-SEP-2002
LOCUS	Homo sapiens voltage-gated calcium channel alpha(2)delta-4 subunit				
DEFINITION	mRNA, complete cds.				
ACCESSION	AF516695				
VERSION	AF516695.1				
KEYWORDS	GI:22770593				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 4604)				
AUTHORS	Qin, N., Vogel, S., Momplaisir, M.L., Codd, E.E. and D'Andrea, M.R.				
TITLE	Molecular Cloning and Characterization of the Human Voltage-Gated Calcium Channel alpha(2)delta-4 Subunit				
JOURNAL	Mol. Pharmacol. 62 (3), 485-496 (2002)				
MEDLINE	22169250				
PUBMED	12181424				
REFERENCE	2 (bases 1 to 4604)				
AUTHORS	Qin, N., Vogel, S., Momplaisir, M.L., Codd, E.E. and D'Andrea, M.R.				
TITLE	Direct Submission				
JOURNAL	Submitted (29-MAY-2002) Drug Discovery, Johnson & Johnson				
FEATURES	Pharmaceutical Research and Development L.L.C., McKean & Welsh				
source	Roads, Spring House, PA 19477, USA				
	Location/Qualifiers				
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		Db		1486	CAAGCCCTCAGAGAAGCCCTCCAGATCTCTGAAGCAGTTCCAAGAGGCCAAGCAAGAAC	1545
		Qy		331	LeuCysAsnGlnAlaIleMetIleLeuSerAspGlyAlaValGluAspTyrGluProVal	350
		Db		1546	CTCTGCAACAGCGCCATCATGTCTCATCAGCAGCGCGCTGGAGGACTACGAGCCGGTG	1605
		Qy		351	PheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArg	370
		Db		1606	TTTGAGAGTATAACTGTGGCCAGACTGTAAAGTCCGAGTCTTCTACTTACCTCATTTGGAGA	1665
		Qy		371	GluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThr	390
		Db		1666	GAAGTGTCTTTTGTGACCGCATGAAGTGGATTGTCATCAACCAACAAAGGCTACTACAG	1725
		Qy		391	GlnIleSerThrIleAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer	410
		Db		1726	CAGATCTCAACGCTGGCGGACACCCAGAGAGAACGTGATGGAATACCTGCACGCTCAGC	1785
		Qy		411	ArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSer	430
		Db		1786	CGCCCCATGGTCATCAACCCAGCCACGACATCATCTGGACAGAGCCCTACATGGACAGC	1845
		Qy		431	LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProVal	450
		Db		1846	AAAGTCTCTCAGCTCGCAGGCTCAGACCTGACACTGCTCACCATGTGGCCATGCCAGTC	1905
		Qy		451	PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp	470
		Db		1906	TTCAGCAAGAAGAACGAAACGCGATCCCATGGCATTTCTCTGGGTGGTGGGCTCAGAT	1965
		Qy		471	ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr	490
		Db		1966	GTGGCCCTCAGAGAGCTGATGAAGCTGGCGCCCCGGGTACAGCTTGGAGTGCACGGATAC	2025
		Qy		491	AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr	510
		Db		2026	GCCTTTCTGAACACCAACAATGGCTACATCTCTCCATCTCCGACCTCCGCGCCCTGTAC	2085
		Qy		511	ArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal	530
		Db		2086	AGAGAGGGGAAGAAATATAAATCCCAACCTAACTACACAGTGTGATCTCTCCGAAGTG	2145

ORIGIN

Alignment Scores:			
Pred. No.:	0	Length:	4604
Score:	5399.50	Matches:	1037
Percent Similarity:	97.65%	Conservative:	4
Best Local Similarity:	97.28%	Mismatches:	25
Query Match:	94.30%	Indels:	1
DB:	9	Gaps:	0
US-09-833-222A-10 (1-1090) x AF516695 (1-4604)			
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Qy	31	TyrSerGlySerLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle	50
Db	646	TACTCAGGCTCTCTCTGCTGCAGAGAAGTACAAGGATGTGGAGTCCAGTCTGAAGATC	705
Qy	51	GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu	70
Db	706	GAGGAGGTGGATGGCTTGGAGCTGGTGAGAGATTTCTCAGAGGACATGGAGAACATGCTG	765
Qy	71	ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn	90
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Qy	91	HisGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArg	110
Db	826	CACGAATTCAATGAATCCCTGGTGTTCGACTATTACAACTCCGCTCCTGATCAACGAGAGG	885
Qy	111	AspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHis	130
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Qy	131	PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr	150
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1606	TTTGTAGAAGTATAACTGGCCAGACTGTAAAGTCCGAGTCTTTCCTTACCTCATTTGGGAGA	1665
371	GluValSerPheAlaAspArgMetLysTrpIleAlaCyAsnAsnLysGlyTyrTyrThr	390
1666	GAAGTGTCTTTTGTGTCAGCCGATGAAGTGGATTGATGCAACAACAAGGCTACTACAG	1725
391	GlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer	410
1726	CAGATCTCAACGCTGGCGGACACCAGGAGAACGTGATGGAAATACCTGCGACGTCTCAGC	1785
411	ArgProMetValIleAsnHisAspHisAspIleIleTprThrGluAlaTyrMetAspSer	430
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Db 3765 ACTCTCGCGGTGACACCA 3782
RESULT 2
BD248445
LOCUS Alpha-2/delta gene.
DEFINITION BD248445
ACCESSION BD248445
VERSION 1 GI:33058215
KEYWORDS JP 2002526100-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 5073)
AUTHORS Johns, M.A., Moldover, B. and Offord, J.D.
TITLE Alpha-2/delta gene
JOURNAL Patent: JP 2002526100-A 3 20-AUG-2002;
WARNER LAMBERT CO
COMMENT OS Homo sapiens (human)
PD JP 2002526100-A/3
PF 07-OCT-1998 JP 2000574561
PR 07-OCT-1998 US 60/103322, 30-OCT-1998 US 60/106473 PR
29-DEC-1998 US 60/114088
PI MARGARET ANN JOHNS, BRIAN MOLDOVER, JAMES DAVID OFFORD PC
C12N15/09, A61K31/711, A61K38/00, A61P25/06, A61P25/08, PC
A61P25/16,
PC A61P25/20, A61P25/22, A61P25/28, A61P25/30, A61P29/00, A61P35/00,
PC C07K14/47,
PC C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12Q1/
02, C12Q1/68,
PC G01N33/15, G01N33/50, C12N15/00, C12N5/00, A61K37/02 CC
Alpha-2/delta gene
FH Key Location/Qualifiers
FT source 1..5073

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Best Local Similarity:	97.09%	Mismatches:	27					
Query Match:	94.07%	Indels:	1					
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US-09-833-222A-10 (1-1090) x BD248445 (1-5073)								
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Qy	31	TyrSerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle	50					
Db	234	TACTCAGGCTCTCTTCTGTCGAGAAGAAGTACAAAGGATGTGGAGTCCAGTCTGAAGATC	293					
Qy	51	GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu	70					
Db	294	GAGGAGTGGATGGCTTGGAGCTGGTGAAGATTTCTCAGAGGACATGGGAACATGCTG	353					
Qy	71	ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn	90					
Db	354	CGCAGGAAAGTCGAGGCGGTCAGAACTCTGGTGGNAGCTGCCGAGGAGCGCCTGAAAC	413					
Qy	91	HisGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuLeuLeuLysLys	110					
Db	414	CACGAATTCAATGAATCCCTGGTGTTCGACTATTACAACTCGGTCCTGTATCAACGAGAG	473					
Qy	111	AspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHis	130					
Db	474	GACGAGAGGGCAACTTCGTGGAGCTGGGCGCGAGTTCTCTCGAGTCCAATGCTCAC	533					
Qy	131	PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr	150					
Db	534	TTCAGCAACCTGCCGGTGAACACCTCCATCAGCAGCGTGCAGCTGCCACCAACGTGTAC	593					
Qy	151	AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe	170					
Db	594	AACAAAGACCCAGATATTTTAAATGGAGTCTACATGTCGAAAGCCTTGAATGCTGCTTC	653					
Qy	171	ValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGly	190					
Db	654	GTGGAGAACTTCCAGAGAGACCCCAACGTTGACCTGGCAATATTTTGGCAGTGAACCTGGA	713					
Qy	191	PhePheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPhe	210					
Db	714	TTCTTCAGGATCTATCCAGGTATAAATGGACACCTGATGAGAAATGGAGTCAATTACTTTT	773					
Qy	211	AspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIle	230					
Db	774	GACTGCCGAAACCGCGGCTGTACATTCAAAGCTGTACTTCTCCCAAGGACATAGTGATT	833					
Qy	231	LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle	250					
Db	834	TTGGTGGACGTGAGCGGCAGTATGAAGGGGCTGAGGATGACTATTGCGCAAGCACCATC	893					
Qy	251	ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp	270					
Db	894	ACCACCATCTTGGACACCTCGGCGGAGAAATGACTTCTGTTAATATCATAGCTCAATGAC	953					
Qy	271	TyrValHisTyrIleGluProCysPheLysGlyLeuValGlnAlaAspArgAspAsn	290					
Db	954	TACGTCAATTACATCGAGCTTGTGTTTAAAGGGATCCTCGTCAGGCGGACCGAGACAAAT	1013					

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ORIGIN

Alignment Scores:

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Percent Similarity:	97.28%	Conservative:	4
Best Local Similarity:	96.90%	Mismatches:	29
Query Match:	93.84%	Indels:	1
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US-09-833-222A-10 (1-1090) x HSM805741 (1-5359)

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Qy	31	TyrSerGlySerLeuLeuGlnLysTyrLysAspValGluSerSerLeuLysValle	50
Db	515	TACTCAGGCTCTCTCTGCTGCAGAAAGTACAAAGGATGTGAGTCCAGTCTGAAGATC	574
Qy	51	GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu	70
Db	575	GAGGAGTGGATGGCTGGAGCTGGTGAGGAAGTTCTCAGAGGACATGGAGAACATGCTG	634
Qy	71	ArgArgLysValGluAlaValGlnAsnLeuValGluAlaGluGluAlaAspLeuAsn	90
Db	635	CGAGGAAAGTCGAGGCGGTCCAGAAATCTGGTGGAAAGTCCGCGAGGAGCGCCCTGAAC	694
Qy	91	HieGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuLleAsnGluArg	110
Db	695	CACGAATTCATGNAATCCCTGGTGTTCCACTATTACAACTCGGTCTGTATCAACGAGAG	754
Qy	111	AspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHis	130
Db	755	GACGAGAAGGCAACTTCGTGGAGCTGGCGCCGAGTTCTCCTGGAGTCCAATGCTCAC	814
Qy	131	PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr	150
Db	815	TTTCAGCAACTGCGCGGTGAACACCTCCATCAGCAGCGTGCAGCTGCCACCAACGTTAC	874
Qy	151	AsnLysAspProAspLleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe	170
Db	875	AACAAAGACCAGATATTTAAATGGAGTCTACATGTTCTGAAGCTTTGAATGCTGCTTC	934
Qy	171	ValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGly	190
Db	935	GTGGAGAACTTCCAGAGAGACCCAAACGTTGACCTGGCAATATTTTGGCAGTGCACCTGA	994
Qy	191	PhePheArgLleTyrProGlyLleLysTrpThrProAspGluAsnGlyValIleThrPhe	210
Db	995	TTCTTCAGATCTATCCAGGTATAAAATGGACACCTGATGAGAATGGAGTCATTTACTTTT	1054
Qy	211	AspCysArgAsnArgGlyTyrTrpIleGlnAlaThrSerProLysAspLleValle	230
Db	1055	GACTGCCAAACCGCGCTGGTACATTCAGCTGCTACTTCTCCCAAGGACATAGTGATT	1114
Qy	231	LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle	250

Db	1115	TTGGTGGACGCTGAGCGGCAGTAGTAAGAGGGCTGAGGATGACTATTGCCAAGCACACCATC	1174
Qy	251	ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp	270
Db	1175	ACACCATCTTGGACACCCCTGGGGGAGAATGACTTCGTTAAATATCATAGCGTACAATGAC	1234
Qy	271	TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn	290
Db	1235	TAGTCCATTACATCCAGCCTTGTTTTAAAGGGATCCTCGTCCAGCGGACCCGAGACAAT	1294
Qy	291	ArgGluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAsp	310
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Qy	311	GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer	330
Db	1355	CAAGCCTTGAGAGAAGCCTTCCAGATCCTGAAGCAGTTCGAAGGGCCCAAGCAAGGAAGC	1414
Qy	331	LeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal	350
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Qy	351	PheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArg	370
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Qy	371	GluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThr	390
Db	1535	GAAGTGTCTTTTGTCTGACCGCATGAAGTGGATTGTCATGCAACCAAGAGGCTACTACACG	1594
Qy	391	GlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer	410
Db	1595	CAGATCTCAACGCTGGCGGACACCCAGGAGAACGTGATGGAATACCTGCACGCTGCTCAGC	1654
Qy	411	ArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSer	430
Db	1655	CGCCCCATGGTCTATCAACCCAGCACGACATCATCTGGACAGAGGCTTACATGGGACAGC	1714
Qy	431	LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProVal	450
Db	1715	AGCTCCTCAGCTCGCAGGCTCAGACCTGACACTGACACTGCTCACCACCTGGGCGCATGCCAGTC	1774
Qy	451	PheSerLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp	470
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Qy	471	ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr	490
Db	1835	GTGGCCCTGAGAGAGCTGATGAAGCTGGCGCCCCGTACAAAGCTTGGAGTGCAACGGATAC	1894
Qy	491	AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr	510
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Qy	511	ArgGluGlyLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal	530
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Qy	531	GluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr	550
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Qy	551	LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn	570
Db	2075	CTCTCGATGATGTGAAGGTTCGATGGATGAAGGAAGCGAGTTCTTTTCTTGACCAAT	2134
Qy	571	AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg	590
Db	2135	GACTACTTCTTCACGACATCAGCGACACCCCTTTTTCAGTTTGGGGGTGGTGTCTGCCGG	2194
Qy	591	GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu	610
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ACCESSION AX098927
VERSION AX098927.1 GI:13538144
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Brown, J.P. and Bertelli, P.
TITLE Secreted soluble_g(a)2_g(d)-2, g(a)2_g(d)-3 or_g(a)2_g(d)-4
calcium channel subunit polypeptides and screening assays using
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JOURNAL Patent: WO 0119870-A 52 22-MAR-2001;
WARNER-LAMBERT COMPANY (US)
FEATURES
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Score: 5342.50 Matches: 1028
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Best Local Similarity: 97.35% Mismatches: 8
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REFERENCE 1
AUTHORS Bertelli,F., Brown,J.P., Dissanayake,V., Suman-Chauhan,N. and
Gee,N.S.
TITLE Screening for alpha2delta-1 subunit binding ligands
JOURNAL Patent: WO 0120336-A 52 22-MAR-2001;
WARNER-LAMBERT COMPANY (US)
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AUTHORS Brown, J.P. and Bertelli, F.
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DEFINITION Sequence 51 from Patent WO0120336.
ACCESSION AX099346
VERSION AX099346.1 GI:13538489
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Bertelli, F., Brown, J.P., Dissanayake, V., Suman-Chauhan, N. and Gee, N.S.
TITLE Screening for alpha2delta-1 subunit binding ligands
JOURNAL Patent: WO 0120336-A 51 22-MAR-2001;
WARNER-LAMBERT COMPANY (US)
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AUTHORS	1 (bases 1 to 5001)		
TITLE	Johns, M.A., Moldover, B. and Offord, J.D.		
JOURNAL	Alpha-2/delta gene		
COMMENT	Patent: JP 2002526100-A 12 20-AUG-2002; WARNER LAMBERT CO		
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REFERENCE 1 (bases 1 to 5960)
AUTHORS Bloeker,H., Boecker,M., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
Fobo,G., Han,M. and Wiemann,S.
TITLE Direct Submission
JOURNAL Submitted (16-JUN-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GSF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKF2p686A1395) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
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ORIGIN

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US-09-833-222A-10 (1-1090) x HSM805740 (1-5960)

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RESULT 10
BD248455
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

BD248455
Alpha-2/delta gene.
BD248455
BD248455.1 GI:33058225
JP 2002526100-A/13..

5712 bp DNA linear PAT 17-JUL-2003

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 5712)
AUTHORS Johns, M.A., Moldover, B. and Offord, J.D.
TITLE Alpha-2/delta gene
JOURNAL Patent: JP 2002526100-A 13 20-AUG-2002;
WARNER LAMBERT CO
COMMENT OS Homo sapiens (human)
PN JP 2002526100-A/13
PD 20-AUG-2002
PF 07-OCT-1999 JP 2000574561
PR 07-OCT-1998 US 60/103322,30-OCT-1998 US 60/106473 PR
29-DEC-1998 US 60/114088
PI MARGARET ANN JOHNS, BRIAN MOLDOVER, JAMES DAVID OFFORD PC
C12N15/09,A61K31/11,A61K38/00,A61K48/00,A61P25/06,A61P25/08, PC
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PC 02,C12Q1/68
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DEFINITION Sequence 50 from Patent WO0119870.
ACCESSION AX098925
VERSION AX098925.1 GI:13538142
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Brown,J.P. and Bertelli,P.
TITLE Secreted soluble g(a)2_g(d)-2, g(a)2_g(d)-3 or g(a)2_g(d)-4
calcium channel subunit polypeptides and screening assays using
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JOURNAL Patent: WO 0119870-A 50 22-MAR-2001;
WARNER-LAMBERT COMPANY (US)
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QY 934 sSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrProValPh 954
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QY 954 eValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLy 974
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QY 974 sValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuValThrAspProTh 994
Db 3114 GGTATTTGTGTGACAGAGATCCCAACAGTAACCTCTCTCTGTGTGACAGACCCAC 3173
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RESULT 12
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LOCUS AX099345
DEFINITION Sequence 50 from Patent WO0120336.
ACCESSION AX099345
VERSION AX099345.1 GI:13538488
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Bertelli, F., Brown, J. P., Diesanayake, V., Suman-Chauhan, N. and Gee, N. S.
TITLE Screening for alpha2delta-1 subunit binding ligands
JOURNAL Patent: WO 0120336-A 50 22-MAR-2001;
WARNER-LAMBERT COMPANY (US)
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Best Local Similarity: 97.92% Mismatches: 3
Query Match: 89.91% Indels: 17
DB: 6 Gaps: 1

US-09-833-222A-10 (1-1090) x AX099345 (1-3201)

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QY 31 TyrSerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
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QY 51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
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QY 111 AspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHis 130
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QY 151 AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe 170
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DEFINITION AX302028
ACCESSION AX302028.1 GI:17383000
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Reddy, R., Thornton, M., Boroweky, M.L., Tang, Y.T., Khan, F.A.,
Tribouley, C.M., Gandhi, A.R., Yao, M.G., Sanjanwala, M.S.,
Baughn, M.R., Nguyen, D.B., Policky, J.L., Yue, H., Seilhamer, J.J.,
Walia, N.K., Lal, P., Kearney, L., Walsh, R.T., Lu, D.A., Greene, B.D.,
Raumann, B.E. and Patterson, C.
JOURNAL Patent: WO 017174-A 27 18-OCT-2001;
Incyte Genomics, Inc. (US)
FEATURES Location/Qualifiers
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DEFINITION Mus musculus (house mouse)
ACCESSION AJ010949
VERSION 1 GI:4186072
KEYWORDS calcium channel alpha-2-delta-C subunit.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Klugbauer, N., Lacinova, L., Marais, E., Hobom, M. and Hofmann, F.
TITLE Molecular diversity of the calcium channel alpha2delta subunit
JOURNAL J. Neurosci. 19, 648-691 (1999)
REFERENCE 2 (bases 1 to 3710)
AUTHORS Klugbauer, N.
TITLE Direct Submission
JOURNAL Submitted (10-SEP-1998) Klugbauer N., Institut fuer Pharmakologie
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und Toxikologie, Technische Universitaet Muenchen, Biedersteiner
Str. 29, 80802, GERMANY
FEATURES
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RESULT 15
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DEFINITION Rattus norvegicus calcium channel alpha-2 delta-3 subunit mRNA,
complete cds.
VERSION AF486278
XREF GI:27450707
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Rattus.
REFERENCE 1 (bases 1 to 3276)
AUTHORS Chu, P.-J. and Best, P.M.
TITLE Molecular cloning of calcium channel alpha (2) delta-3 subunits from
rat atria and the differential regulation of their expression by
IGF-1
JOURNAL J. Mol. Cell. Cardiol. 35 (2), 207-215 (2003)
MEDLINE 22494975
PUBMED 12606261
REFERENCE 2 (bases 1 to 3276)
AUTHORS Chu, P.-J. and Best, P.M.
TITLE Direct Submission
JOURNAL Submitted (19-FEB-2002) Department of Molecular and Integrative
Physiology, University of Illinois, 407 S. Goodwin Ave., Urbana, IL
61801, USA
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GenCore version 5.1.6
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SUMMARIES

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ALIGNMENTS

RESULT 1

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; Sequence 18, Application US/10162012
; Patent No. 6682597
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
; FILE REFERENCE: 10448-190001
; CURRENT APPLICATION NUMBER: US/10/162,012
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/875,321
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18398
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,238
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,363
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18247
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/227,068
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 09/928,530
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/25475
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: US 60/226,770
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; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 10/109,029
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; PRIOR APPLICATION NUMBER: PCT/US02/09728
; PRIOR FILING DATE: 2002-03-28
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; PRIOR APPLICATION NUMBER: US (not assigned)
; PRIOR FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 1091
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-162-012-18

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Best Local Similarity 60.0%; Pred. No. 0;
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; Patent No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
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; SEQ ID NO 24
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Query Match      59.7%; Score 3419.5; DB 4; Length 1077;
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QY 73 KVEAQNVLVEAAEADLNHEFNEISLVFYDYNVSLINERDEKGNFVELGAELLESNAHFS 132
Db 102 KSEAVRVLVEAAEAEHLKHEFDADLQYEFYFNAVLINERDKGNFLELGKEFILAPNDHFN 161
QY 133 NLPVNTSISSVOLPTNVYKNDPDLNGVYMSALNAVVENFORDPDLTWQYFGSATGPF 192
Db 162 NLPVNTISLSDVQVPTNMVYKNDPAIVNGVYMSLSLNVFVDFNDRDPSLIWQYFGSAKGF 221
QY 193 RIYPGKWTDPENGVTTFDCRNRGWYIOAATSPKDIIVLDVSGSMKGLRMTIAKHTIT 252
Db 222 RQYPGIKWEPDENGVTAFDCRNRKWIYIOAATSPKDVILVDVSGSMKGLRMTIAKQT VSS 281
QY 253 ILDTLGENDFVNIAYNDYVHYIEPCFKGILVQADRDNREHFKLLVEELMVKGVVDOA 312
Db 282 ILDTLGDGDDFNIIYNEELHYVEPCNLGTLVQADRTNKEHFRHLDKLFAGIGMLDIA 341
QY 313 LREAFQILKQFOBAKQSGSLCNOAIMLISDGAVEDYEPVPEKYNWPKCKVRVFTYLIGREV 372
Db 342 LNEAFNILSDFNHTGOGSICSOAIMLITDGAVDYDTIFAKYNWPKCKVRIFTYLIGREA 401
QY 373 SPADRMKWIACNKGYYTQISTLADTOENVMYELHVLSPRMVNHDDIITWTEAYWDSKL 432
Db 402 AFADNLKMACANKGFFTOISTLADVQENVMYELHVLSPRKVIDQBDHVVWTEAYIDSTL 461
QY 433 LSSQA-----QSLTLTLTVAMPVFSKKNETRSHGILLGVGSDVALRELKMLAPRYKLGVH 488
Db 462 POAQKLADDOGLVMTTAVMPVFSKQNETSKGILLGVGVDTPVVKELTKIPYKLGIIH 521
QY 489 GYAFPLTNNGYIILSHDPLRLPYREGKKLKPKNYNSVDLSEWEDEQASLRTAMINRET 548
Db 522 GYAFAITNNGYIILTHPELRPLYEEGKK-RRKPNYSVDLSEWEDEDRDDVLRNAMYNRKT 580
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Qy	667	VVTPAMEAYWTALANMSESEHVVWNAFVIGTRAGLLRSSLFVGESEKVSORKFVLTPPDEA	726
Db	699	WSAPIEAYWTSALNSENSEKDGVEAFVAFVTRTGLSRINLFLVGAEOULTNQDFLKAQDKE	758
Qy	727	SVFTLDRFPFLWYRQASRHPAGSVFVFNLRWAEGPESAGEPMVVTASTAVATVVKRTAIAA	786
Db	759	NIFNADHFPFLWYRRAAQIPGSFVYISIPFSTGP--VNKSNVVVTAFTSIQLLDERKSPVA	816
Qy	787	AAGVQMKEFLQRFKFWAATQCSTVWDGPPYQTQSCSDSLDCFVIDNNNGFILISKRSRETR	846
Db	817	AVGIQMKLEFFQRFKFWTASRQASLDGKCSISCDDETVNVCYLIDNNNGFLLVSEDYTQTGD	876
Qy	847	FLGEVDGAVILTQLLSMGVFGQVWYDYQAMCKSPSSHHSAAQPLVSPISAFPLFATRWLLQ	906
Db	877	FFGEIEGAVNKKLITMGVSFKRITLYDYQAMCRANKESSDGAHGLLDYPNAFLSAVKWIMT	936
Qy	907	ELVLFLLEWSVWGSWYDRGAEAKSVFHHSHKKQDFLQPCDTEYPVYVQPAIREANGI	966
Db	937	ELVLFLVEFNLC-SWHSMDMTAKA-----QKLQKTFEPCDTEYPFAVSERTIKETGNN	988
Qy	967	VEGCPCKQVFWVOQIPNSNLLLLLVTDPTCDCSFPPLVQEBATEVKYVNASVKCDRMRSOKL	1026
Db	989	IACEDCSKSFVQIQIPSNLFPMVVDSSCLICESVAPITMAPIEIRYNESLKCERLKAQKI	1048
Qy	1027	RRRPDSCHAFHPE	1039
Db	1049	RRRPESCHGFHPE	1061

RESULT 4

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US-09-397-550-12
; Sequence 12, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 1065
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-397-550-12

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Qy	313	LR	AF	QIL	K	Q	B	A	K	G	S	L	C	N	Q	A	I	M	L	S	D	G	A	V	E	D	Y	E	P	V	F	E	K	Y	N	P	D	C	K	V	R	V	F	T	L	I	G	R	E	V	372								
Db	342	L	N	E	A	F	N	I	L	S	D	F	N	H	T	G	G	S	I	C	S	A	I	M	I	T	D	G	A	V	T	D	T	I	F	A	K	Y	N	P	D	R	K	V	R	I	F	T	L	I	G	R	E	A	401				
Qy	373	S	F	A	D	R	M	K	W	I	A	C	N	K	Y	T	O	I	S	T	L	A	D	T	O	E	N	V	M	E	Y	L	H	V	L	S	R	P	M	V	I	N	H	D	I	I	T	W	E	A	Y	M	D	S	K	L	432		
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Qy	433	L	S	S	O	A	O	S	L	T	L	T	V	A	M	P	V	F	S	K	Q	N	E	T	R	S	H	G	I	L	L	G	V	G	S	D	V	A	L	R	M	K	L	A	P	R	K	L	G	V	H	G	Y	A	F	492			
Db	462	T	D	D	O	G	P	--	V	L	M	T	V	A	M	P	V	F	S	K	Q	N	E	T	R	S	K	G	I	L	L	G	V	G	T	D	V	P	K	E	L	L	T	I	P	K	Y	L	G	I	H	G	Y	A	F	519			
Qy	493	L	N	T	N	G	V	I	L	S	H	P	D	I	R	P	L	Y	R	E	G	K	L	K	P	K	N	Y	S	V	D	L	S	E	V	E	D	Q	A	E	S	L	R	T	A	M	I	N	R	E	T	G	T	L	S	552			
Db	520	A	I	T	N	G	Y	I	L	T	H	P	E	L	R	L	L	Y	E	E	G	K	--	R	R	K	P	S	S	V	D	L	S	E	V	E	D	R	D	D	V	L	R	N	A	M	V	A	R	K	T	G	F	S	578				
Qy	553	M	D	V	K	P	M	D	K	G	R	V	L	F	L	T	N	D	Y	F	F	T	D	I	S	D	T	P	S	I	C	A	N	L	S	R	G	H	E	Y	I	L	L	C	N	T	S	V	E	S	G	L	H	D	L	L	H	612	
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Db	639	P	D	V	S	L	A	D	E	W	S	C	N	T	D	L	H	P	E	R	H	L	S	O	L	E	A	I	K	L	K	G	K	E	P	L	L	O	C	D	K	E	L	I	Q	E	V	L	F	D	A	V	S	A	P	I	698		
Qy	673	E	A	Y	T	A	L	A	L	N	K	S	E	S	H	V	D	M	A	F	I	G	T	R	A	G	L	L	R	S	L	F	V	G	S	K	V	S	D	R	K	P	L	T	D	E	E	A	S	V	T	L	D	732					
Db	699	E	A	Y	M	T	S	L	A	L	N	S	N	S	K	G	V	E	A	F	L	G	T	R	I	T	G	L	S	R	I	N	L	F	V	G	A	E	L	N	Q	D	F																

RESULT 5

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US-09-397-550-22
; Patent 22, Application US/09397550
; Sequence No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 22
; LENGTH: 1085
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-397-550-22

```

Query Match		59.6%; Score 3410.5; DB 4; Length 1085;
Best Local Similarity		60.3%; Pred. No. 0;
Matches		619; Conservative 188; Mismatches 207; Indels 13; Gaps 5;
Qy	13	VKLWADTFGGDLVNTVTYKSGSLLLQKKYKDVSSLLKIEBVDGLVLRKSEDMENMLRR 72
Db	42	VKLWASAFGGEIISIAAKYSGSLQKKYKEYEKDVAIEIDGLQLVKLAKMEENFHK 101
Qy	73	KVEAVQNLVBAABEADLNHFEBSLVDPYNSVLINERDEKGNFVELGAEFLLESNAHFS 132
Db	102	KSEAVRRLVEABEEAHLKHEFDADLOVEYFNAVLINERDKGNFLELGKSFILAPNDHN 161
Qy	133	NLPVNTSISVQLPTNVYKDPDILNGVYMSALNAVVENFQDPTLTWQYFGSATGFF 192
Db	162	NLPVNTSLSDVQVPTMYNKDPAIVNGVYMSLSLNVFVDFNDRPDSLWQYFGSAKGF 221
Qy	193	RIYPGKWTDPENGVIPTFCRNRGWYIOAATSPKDIVILVDVSGSMKGLRMTAKHTITT 252
Db	222	RQYPGIKWEPDENGVIATFCRNKRWYIOAATSPKDVVILVDVSGSMKGLRLTTAKQTSS 281
Qy	253	ILDTLGENDFNIIAYNDYVHYIEPCFKGILVQADRNRHEFKLLVBEELMVGKGVVDQA 312
Db	282	ILDTLGDDDFNIIAYNEELHYVEPCNLGTLVQADRTNKEHFEHLDKLFAKGIGMLDIA 341
Qy	313	LREAFQILKQFOEAKQSGSLCNQAIMLISDGAVEDYEPVEKYNWPDCKVRVFTYLIGREV 372
Db	342	LNEAFNLSDFNHTGGSGISCSQAIMLITDGAVDYDTIFAKYNWPDCKVRIFTYLIIGREA 401
Qy	373	SPADRMKWIACNNKGYTQISTLADTOENVMYELHVLSPRMVINHDHDIITWEAYMDSKL 432
Db	402	AFADNLKWMACANKGFFQTISTLADVOENVMYELHVLSPRPKVIDQEHVVWTEAYIDSTL 461
Qy	433	LSSQAQSLTLTTVAMPVFSKKNETRSKGILLGWGTVDPVKELKTIIPKYKLGIGHYAF 492
Db	462	TDDQGP--VLMTTVAMPVFSKQNETRSKGILLGWGTVDPVKELKTIIPKYKLGIGHYAF 519
Qy	493	LNTNNGYILSHDPLRPLRYREGKLLKPKPNYNSVDLSEVEDOQAESLRITAMINRETGTL 552
Db	520	AITNNGYILTHPELRLLYBEGKK--RRKPNYSVDLSEVEDEDRDDVLNRNANVRKTKGFS 578
Qy	553	MDVKVPMDKGRVLFNTNDYFTDISDTPFSLGAVLSRGHGEYILLGNTSVBEGLDLHL 612
Db	579	MEVKTVDKGRVLMVNDYITDITKGTLPFSLGVALSRGHGKFFFRGNVTIEGLHDLEH 638
Qy	613	PDALAGDWIYICITDIPDHRKLSQLEAMIRFLTRKDPDLECEDEELVREYLFDAVVTAPM 672
Db	639	PDVSLADEWSYCNLDLHPEHRLHLSQLEAIKLYLKGKEPLLQCKELIQEVLFDAVVSAPI 698
Qy	673	EAYWTALANMSESESHVVDMAFLGTRAGLLRSSSLFVGSEKVSDDRFLPEDEASVFTLD 732
Query Match		58.1%; Score 3326.5; DB 4; Length 1038;
Best Local Similarity		60.0%; Pred. No. 0;
Matches		606; Conservative 185; Mismatches 206; Indels 13; Gaps 5;
Qy	13	VKLWADTFGGDLVNTVTYKSGSLLLQKKYKDVSSLLKIEBVDGLVLRKSEDMENMLRR 72
Db	42	VKLWASAFGGEIISIAAKYSGSLQKKYKEYEKDVAIEIDGLQLVKLAKMEENFHK 101
Qy	73	KVEAVQNLVBAABEADLNHFEBSLVDPYNSVLINERDEKGNFVELGAEFLLESNAHFS 132
Db	102	KSEAVRRLVEABEEAHLKHEFDADLOVEYFNAVLINERDKGNFLELGKSFILAPNDHN 161
Qy	133	NLPVNTSISVQLPTNVYKDPDILNGVYMSALNAVVENFQDPTLTWQYFGSATGFF 192
Db	162	NLPVNTSLSDVQVPTMYNKDPAIVNGVYMSLSLNVFVDFNDRPDSLWQYFGSAKGF 221
Qy	193	RIYPGKWTDPENGVIPTFCRNRGWYIOAATSPKDIVILVDVSGSMKGLRMTAKHTITT 252
Db	222	RQYPGIKWEPDENGVIATFCRNKRWYIOAATSPKDVVILVDVSGSMKGLRLTTAKQTSS 281
Qy	253	ILDTLGENDFNIIAYNDYVHYIEPCFKGILVQADRNRHEFKLLVBEELMVGKGVVDQA 312
Db	282	ILDTLGDDDFNIIAYNEELHYVEPCNLGTLVQADRTNKEHFEHLDKLFAKGIGMLDIA 341
Qy	313	LREAFQILKQFOEAKQSGSLCNQAIMLISDGAVEDYEPVEKYNWPDCKVRVFTYLIGREV 372
Db	342	LNEAFNLSDFNHTGGSGISCSQAIMLITDGAVDYDTIFAKYNWPDCKVRIFTYLIIGREA 401
Qy	373	SPADRMKWIACNNKGYTQISTLADTOENVMYELHVLSPRMVINHDHDIITWEAYMDSKL 432
Db	402	AFADNLKWMACANKGFFQTISTLADVOENVMYELHVLSPRPKVIDQEHVVWTEAYIDSTL 461
Qy	433	LSSQAQSLTLTTVAMPVFSKKNETRSKGILLGWGTVDPVKELKTIIPKYKLGIGHYAF 492
Db	462	TDDQGP--VLMTTVAMPVFSKQNETRSKGILLGWGTVDPVKELKTIIPKYKLGIGHYAF 519
Qy	493	LNTNNGYILSHDPLRPLRYREGKLLKPKPNYNSVDLSEVEDOQAESLRITAMINRETGTL 552
Db	520	AITNNGYILTHPELRLLYBEGKK--RRKPNYSVDLSEVEDEDRDDVLNRNANVRKTKGFS 578
Qy	553	MDVKVPMDKGRVLFNTNDYFTDISDTPFSLGAVLSRGHGEYILLGNTSVBEGLDLHL 612
Db	579	MEVKTVDKGRVLMVNDYITDITKGTLPFSLGVALSRGHGKFFFRGNVTIEGLHDLEH 638
Qy	613	PDALAGDWIYICITDIPDHRKLSQLEAMIRFLTRKDPDLECEDEELVREYLFDAVVTAPM 672
Db	639	PDVSLADEWSYCNLDLHPEHRLHLSQLEAIKLYLKGKEPLLQCKELIQEVLFDAVVSAPI 698
Qy	673	EAYWTALANMSESESHVVDMAFLGTRAGLLRSSSLFVGSEKVSDDRFLPEDEASVFTLD 732
Db	699	EAYWTSIALNKSNSDKGVEVAFGLTRTGLSRINLFGABQLTNQDPLKAGDKENIFNAD 758
Qy	733	RPLWYRQASEHPAGSPVFNLRWABGPESAGEPMVYTTASTAVVTDKRTAIAAAGVOM 792
Db	759	HFPLWYRRAAQIPGSPVYIPISTGP--VNKNVVTASTSIQLDERKSPVVAAGIQM 816
Qy	793	KLBFLOKFWAARTQCSPTQSDGPTQSCEDSDLCFCFVDNNGFFILISKRSETGRFLGEVD 852
Db	817	KLFEFFQKFWASRQCASLDGKCSISCDDETVCYLLDNNGFILVSEDYTQTGDFGGEIE 876
Qy	853	GAVLITQLLSMGVSQVMTYDQAMCKPSSHHAQAQLVSPISAFLTATRWILOELVFL 912
Db	877	GAVNMKLLTWGSPKRIITLYDQAMCRANKSSSDGAHGLDLPYNAFLSAVKWIMTELVLFL 936
Qy	913	LEWSVMSWYDRGAESVPHSHKHKKQDPLQPCDTEYFVYVYOPAIRANGIVEGCP 972
Db	937	VEFNLC--SWHSDMTAKA-----QKLKOTLPCDTEYFPAFVSERTIKETTGNACEDC 988
Qy	973	QKVFVVOQIIPNSLLLVTDPTDCSIFPPVLOEATEVKYNASVCDRMRSQKLRRPDS 1032
Db	989	SKSFVIOQIPSSNLFMVVDSSCLCESVAPITWAPIEIRYNESLKCRKAQKIRRPES 1048
Qy	1033	CHAFHPE 1039

Db 699 EAYWTSALNKSSENSDKGEVAFGLTRTGLSRINLFGAQLTNQDPLKAGDKENIPNAD 758
Qy 733 RFPLWYQASEHPAGSFVFNLRWAEQGESAGPMVVTASTAVAVTVDKRTAIAAAAGVQM 792
Db 759 HFPLWYRAAEQIPGSEVYISPFSTGP--VNKSNVVTASTSIQLDERKSPVVAAGVQM 816
Qy 793 KLEFLQKFWAATQRCSTVDGPTQSCDSDLDGCFVLDNNGFFILISKRSRETGRFLGEVD 852
Db 817 KLEFFQKFWTASRQACASLGKCSICDDETVCYLIDNNGFFILVSEDTYQTGDFGGEIE 876
Qy 853 GAVLTQLLSGVFSQVMTYDYQAMCKPSSHHSAAQPLVSPISAFLTATRWLLQELVFL 912
Db 877 GAVMKNLLTWSFKRITLYDYQAMCRANKESSDGAHGLDPPYNAFLSAVKWIMTELVLFL 936
Qy 913 LEWSVMSWYDRGAESVHHSHKHKQDPLQPCDTEYFVYQPAIREANGIVECGPC 972
Db 937 VEFNLC-SWVHSDMTAKA-----QKLKQTLPCDTEYFVYQPAIREANGIVECGPC 988
Qy 973 QKVFVVOQIPNSNLLLVTDPTDCDSIFPPVLOEATKYNASVKCDRMR 1022
Db 989 SKSFVIQIPSSNLFMVVVDSSCLCESVAPIWTAPTEIRNLSKLERLK 1038
RESULT 7
US-09-397-550-10
; Sequence 10, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1019
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-397-550-10

Query Match 57.3%; Score 3278.5; DB 4; Length 1019;
Best Local Similarity 60.4%; Pred. No. 2.9e-315; Mismatches 200; Indels 13; Gaps 5;
Matches 599; Conservative 179; Mismatches 200; Indels 13; Gaps 5;
Qy 13 VKLWADTFGGDLTYNTVTKYSGSLLQLKKYKDVESLKIIEVDGLVLRKFSDEMNNLR 72
Db 42 VKLWASAFGEIKSIAAKYSGSLLQLKKYKEYEKDVAIEIDGLQVLKLNKWEEMPHK 101
Qy 73 KVAQNVLVEAABEADLNHFENSLVFDYNSVLINERDEKGNFVGLGAFFLLESNAHFS 132
Db 102 KSEAVRRLVEAABEALHKEHFDADLQVEYFNAVLINERDKGNFGLGKEFIFLAPNDHF 161
Qy 133 NLPVNTSISVQLPTVYNNKDPDLNGVYMSALNAVFNENFORDPLTWQYFGSATGPF 192
Db 162 NLPVNTSLSDVQPTTNNKDPALVNGVYMSLSNKVFNDFORDPSLIWYFGSARGF 221
Qy 193 RIYPGKWTDPDNGVITFCRNRGWTQAATSPKDVILVDVSGSMKGLRMTAKITIT 252
Db 222 RQYPGIKWEPDENGVIADFRCNRKWIQAATSPKDVILVDVSGSMKGLRLTIKQTVSS 281
Qy 253 ILDTLGENDFVNIANDVYHYEPCFKGILLVQADRDNRHFKLLVBEELMKVGVVDQA 312
Db 282 ILDTLGDGDDFPNTIAYNEELHYEPCFKGILLVQADRDNRHFKLLVBEELMKVGVVDQA 341
Qy 313 LREAFOILKQFOBAKOGSLCQAIMLISDGAVEDYSPVPEKYNWPKVRYFTYLLIGREV 372
Db 342 LNEAFNLSLDFNHTGGQSCSQAIMLITDGAVDYDTIFAKYNWPKVRYFTYLLIGREV 401
Qy 373 SPADRMKIACNNKGYTQISTLADTQENVMYHLVSLRPMVINHDHDIITWEAYMDSKL 432

Db 402 AFADNLKMWACANKGFTQISTLADVQENVMYHLVSLRPMVINHDHDIITWEAYMDSKL 461
Qy 433 LSSQAQSLTLLTTVAMPVFSKQNETRSHGILLGVGSDVALRMLKLAIPRYKLGIVHGYAF 492
Db 462 TDDQGGP--VLMTTVAAPVFSKQNETRSHGILLGVGSDVALRMLKLAIPRYKLGIVHGYAF 519
Qy 493 LNTNNGYIILSHPDRLRPLYREGKKLPKPNVNSVDLSEVEWEDQAESIRATAMINRETGTL 552
Db 520 AITNNGYIILSHPDRLRPLYREGKKLPKPNVNSVDLSEVEWEDQAESIRATAMINRETGTL 578
Qy 553 MDVKVPMDKGRVFLFTNDYFFTDISDTPFSLGAVLSRSGHEGYILLGNTSVSEGLDHL 612
Db 579 MEVKTVTDGKRVFLVMTNDYVYVTDIKGTPFSLGAVLSRSGHEGYILLGNTSVSEGLDHL 638
Qy 613 PDALAGDWIYCIITDIDPHRKLQLEAMIRFLTRKDPDLECEBELVREVLFDAVVTAPM 672
Db 639 PDVSLADEWSYCNVTDLHPEHRLSQLEAIKLYLKGEPLLCQDKELIQEVLFDVAVSAPI 698
Qy 673 EAYWTALANMSESESHVYDMAFLGTRAGLLRSSLFVSGSEKSDRKLFTLPEDEASVFTLD 732
Db 699 EAYWTSALNKSSENSDKGEVAFGLTRTGLSRINLFGAQLTNQDPLKAGDKENIPNAD 758
Qy 733 RFPLWYQASEHPAGSFVFNLRWAEQGESAGPMVVTASTAVAVTVDKRTAIAAAAGVQM 792
Db 759 HFPLWYRAAEQIPGSEVYISPFSTGP--VNKSNVVTASTSIQLDERKSPVVAAGVQM 816
Qy 793 KLEFLQKFWAATQRCSTVDGPTQSCDSDLDGCFVLDNNGFFILISKRSRETGRFLGEVD 852
Db 817 KLEFFQKFWTASRQACASLGKCSICDDETVCYLIDNNGFFILVSEDTYQTGDFGGEIE 876
Qy 853 GAVLTQLLSGVFSQVMTYDYQAMCKPSSHHSAAQPLVSPISAFLTATRWLLQELVFL 912
Db 877 GAVMKNLLTWSFKRITLYDYQAMCRANKESSDGAHGLDPPYNAFLSAVKWIMTELVLFL 936
Qy 913 LEWSVMSWYDRGAESVHHSHKHKQDPLQPCDTEYFVYQPAIREANGIVECGPC 972
Db 937 VEFNLC-SWVHSDMTAKA-----QKLKQTLPCDTEYFVYQPAIREANGIVECGPC 988
Qy 973 QKVFVVOQIPNSNLLLVTDPTDCDSIFPPV 1003
Db 989 SKSFVIQIPSSNLFMVVVDSSCLCESVAPI 1019
RESULT 8
US-09-397-550-18
; Sequence 18, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-397-550-18
Query Match 31.3%; Score 1792.5; DB 4; Length 350;
Best Local Similarity 97.4%; Pred. No. 1.2e-168;
Matches 341; Conservative 2; Mismatches 6; Indels 1; Gaps 1;
Qy 700 AGLLRSSILFVSGSEKSDRKLFTLPEDEASVFTLDRPFLWYQASEHPAGSFVFNLRWAE 759
Db 1 SGLLRSSILFVSGSEKSDRKLFTLPEDEASVFTLDRPFLWYQASEHPAGSFVFNLRWAE 60
Qy 760 ESAGEPMVVTASTAVAVTVDKRTAIAAAAGVQMKEFLQKFWAATQRCSTVDGPTQSC 819

Db 61 ESAGEPMVVTASTAVAVTVDKRTAIAAAGVQMKLEFLQRFKFWAATRCQSTVDGPTQSC 120
Qy 820 EDSLDLCFVIDNNGFILIISKRSRETGRFLGVDGAVLTQLLSMGVFSQVTMYDYQAMCKP 879
Db 121 EDSLDLCFVIDNNGFILIISKRSRETGRFLGVDGAVLTQLLSMGVFSQVTMYDYQAMCKP 180
Qy 880 SSHHSAAPLVSPISAFATATRWLLQELVLFLEWSVMSWYDRGAEAHSVHHSHKHK 939
Db 181 SSHHSAAPLVSPISAFATATRWLLQELVLFLEWSVMSWYDRGAEAHSVHHSHKHK 240
Qy 940 KQDPLQPCDTEYFVYVQPAIREANGIVEGCPQKVFVWQOIPNSNLLLVLTPTDCDSI 999
Db 241 KQDPLQPCDTEYFVYVQPAIREANGIVEGCPQKVFVWQOIPNSNLLLVLTPTDCDSI 300
Qy 1000 FPPVLQATEVKYNASVKCDRMRSQLRRRPSDCHAFHPVVRVEADRGWA 1049
Db 301 FPPVLQATEVKYNASVKCDRMRSQLRRRPSDCHAFHPVVRVEADRGWA 349

RESULT 9
US-09-397-550-17
; Sequence 17, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-397-550-17

Query Match 29.6%; Score 1695; DB 4; Length 323;
Best Local Similarity 99.4%; Pred. No. 4.9e-159;
Matches 321; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 700 AGLRSSLFVGSEKVSDRKFLTPDEASVFTLDRFPFLWYRQASEHPAGSFVFNLRWAEGP 759
Db 1 SGLLRSSLFVGSEKVSDRKFLTPDEASVFTLDRFPFLWYRQASEHPAGSFVFNLRWAEGP 60
Qy 760 ESAGEPMVVTASTAVAVTVDKRTAIAAAGVQMKLEFLQRFKFWAATRCQSTVDGPTQSC 819
Db 61 ESAGEPMVVTASTAVAVTVDKRTAIAAAGVQMKLEFLQRFKFWAATRCQSTVDGPTQSC 120
Qy 820 EDSLDLCFVIDNNGFILIISKRSRETGRFLGVDGAVLTQLLSMGVFSQVTMYDYQAMCKP 879
Db 121 EDSLDLCFVIDNNGFILIISKRSRETGRFLGVDGAVLTQLLSMGVFSQVTMYDYQAMCKP 180
Qy 880 SSHHSAAPLVSPISAFATATRWLLQELVLFLEWSVMSWYDRGAEAHSVHHSHKHK 939
Db 181 SSHHSAAPLVSPISAFATATRWLLQELVLFLEWSVMSWYDRGAEAHSVHHSHKHK 240
Qy 940 KQDPLQPCDTEYFVYVQPAIREANGIVEGCPQKVFVWQOIPNSNLLLVLTPTDCDSI 999
Db 241 KQDPLQPCDTEYFVYVQPAIREANGIVEGCPQKVFVWQOIPNSNLLLVLTPTDCDSI 300
Qy 1000 FPPVLQATEVKYNASVKCDRMR 1022
Db 301 FPPVLQATEVKYNASVKCDRMR 323

RESULT 10
US-09-397-550-16
; Sequence 16, Application US/09397550
; Patent No. 6783952

; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-397-550-16

Query Match 27.9%; Score 1598; DB 4; Length 304;
Best Local Similarity 99.3%; Pred. No. 1.8e-149;
Matches 302; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 700 AGLRSSLFVGSEKVSDRKFLTPDEASVFTLDRFPFLWYRQASEHPAGSFVFNLRWAEGP 759
Db 1 SGLLRSSLFVGSEKVSDRKFLTPDEASVFTLDRFPFLWYRQASEHPAGSFVFNLRWAEGP 60
Qy 760 ESAGEPMVVTASTAVAVTVDKRTAIAAAGVQMKLEFLQRFKFWAATRCQSTVDGPTQSC 819
Db 61 ESAGEPMVVTASTAVAVTVDKRTAIAAAGVQMKLEFLQRFKFWAATRCQSTVDGPTQSC 120
Qy 820 EDSLDLCFVIDNNGFILIISKRSRETGRFLGVDGAVLTQLLSMGVFSQVTMYDYQAMCKP 879
Db 121 EDSLDLCFVIDNNGFILIISKRSRETGRFLGVDGAVLTQLLSMGVFSQVTMYDYQAMCKP 180
Qy 880 SSHHSAAPLVSPISAFATATRWLLQELVLFLEWSVMSWYDRGAEAHSVHHSHKHK 939
Db 181 SSHHSAAPLVSPISAFATATRWLLQELVLFLEWSVMSWYDRGAEAHSVHHSHKHK 240
Qy 940 KQDPLQPCDTEYFVYVQPAIREANGIVEGCPQKVFVWQOIPNSNLLLVLTPTDCDSI 999
Db 241 KQDPLQPCDTEYFVYVQPAIREANGIVEGCPQKVFVWQOIPNSNLLLVLTPTDCDSI 300
Qy 1000 FPPV 1003
Db 301 FPPV 304

RESULT 11
US-09-470-443-6
; Sequence 6, Application US/09470443
; Patent No. 6441156
; GENERAL INFORMATION:
; APPLICANT: Leiman, Michael I.
; APPLICANT: Minna, John D.
; APPLICANT: Latif, Farida
; APPLICANT: Wei, Ming-Hui
; APPLICANT: Sekido, Yoshitaka
; APPLICANT: Gao, Boning
; APPLICANT: Duh, Fuh-Mei
; TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
; FILE REFERENCE: NIH-05043
; CURRENT APPLICATION NUMBER: US/09/470,443
; CURRENT FILING DATE: 1999-12-22
; EARLIER APPLICATION NUMBER: 60/114,359
; EARLIER FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1076
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-470-443-6

Query Match 20.7%; Score 1183.5; DB 4; Length 1076;
Best Local Similarity 29.6%; Pred. No. 2.7e-107;

Db 533 DIKRLTNYTNGYVFAIDLNGYVLLHPLNPKPQTNNPREPVTL-----DFLDAE 583
Qy 532 WEDQ-ABSLRTAMINRETGTLSMDVKVPMKGRKRVFLTNDYFPTDTSDFPFLSGAVLSR 590
Db 584 LEDENKEIRSMIDGNKGKHQIRTLVKSLDERYIDEVTNRYTWPIRSTNYSGLVLP 643
Qy 591 GHGEYI-----LLGNTSVBEGUHLHPLDALAGOWIYICITIDDPHRK 634
Db 644 YSTFYQANLSDQILQVKYFEFLPSSFESEG-HVFIAPR-----EYC-KOLNASDNN 694
Qy 635 LSQLEAMIRFLTRKDPD-LECDEELVREVLFDVAVTAPM-EAYWTALALNMSESEHVVD 692
Db 695 TEFKXNFIELMEKVTPOSKOCNNFLNLHLLDGTITQQLVERVWRDQDLN-----TVSLL 749
Qy 693 MAFGLTRAGLRSSLFVSGSEKVSDRKFLTPDEASVFTLDRFPL--WYRQASEHPAGSF 749
Db 750 AVFAATDGGITR-----VFNKAEDWTENPEPNASFYRSLDN--HGY 792
Qy 750 VFN-----LRWAGP-ESAGEPMVVTASTAVAVTVDKRTAIAAAAGVQMKLEFLQKRF 801
Db 793 VFKPPHODALLR-----PLELNDTVGILVSTAVELSLGRRTLPRPAAVGVKLDLEAWAEKF 848
Qy 802 WAATROQSTVDGPTQSC-----EDSLDCFVIDNNGFILI SKRSR---ETGR 846
Db 849 KVLASNRTHQDQP--QKCGPNSHCEMDCVNNEDLLCVLIDGGFLVLSNQNHQDQVGR 906
Qy 847 FLGEVDGAVLTQLLSMGVFSQVMTYDQAMCKPSSHHSAAQP---LVSPISAPL----- 898
Db 907 FFEVDANLMLALYNNFSYTRKESYDQAACAPQPPGNLGAAPRGVFPVPTVAFLNLAW 966
Qy 899 -TATRWLLQELVFLLEWSVWGSWYDRG---ABAKSVFHHSHKHKKQDPLQPCDTETYPVF 954
Db 967 TSAAAWSLFQQLLYGL---IYHSWFQADPAEAGSPETRESSCVMKQ-----TQY--- 1013
Qy 955 VYQPAIREA-NGIVECGPCQKVFVQOIPNSNLLLTVD-PTCDCSIFFPVLQEAETVKY 1012
Db 1014 -YFGSVNASYNAIDCNCNRLFHAORLTNLLFVVAEPLCSQCBAGRLLOKETHCPA 1072
Qy 1013 NASVKCDRMRSQKLRRRPDSCAFHPHVRVEADRGWAGFSNPPLCIGLCPCRQ--EHIG 1070
Db 1073 DGEQELVORPRYRGRPHICFDYN-----ATEDSDCGRSGASFPPLSLGLVLSQLLLLG 1128
Qy 1071 MPNMTVPVLLGNIRV 1087
Db 1129 LPPRPOQVLVHASRRL 1145

RESULT 13

US-09-470-443--4
; Sequence 4, Application US/09470443
; Patent No. 6441156
; GENERAL INFORMATION:
; APPLICANT: Lerman, Michael I.
; APPLICANT: Minna, John D.
; APPLICANT: Latif, Farida
; APPLICANT: Wei, Ming-Hui
; APPLICANT: Sekido, Yoshitaka
; APPLICANT: Gao, Boning
; APPLICANT: Duh, Fuh-Wei
; TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
; FILE REFERENCE: NIH-05043
; CURRENT APPLICATION NUMBER: US/09/470,443
; CURRENT FILING DATE: 1999-12-22
; EARLIER APPLICATION NUMBER: 60/114,359
; EARLIER FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1145
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-470-443--4

Query Match 20.7%; Score 1183.5; DB 4; Length 1145;
Best Local Similarity 29.6%; Pred. No. 3e-107;
Matches 343; Conservative 209; Mismatches 436; Indels 169; Gaps 42;
Qy 16 WADTFGGDLTYNTVKYSGSLLQKKYKDVESLLKIEEVDGLKLVKFESEDMENMLREKVE 75
Db 73 WARRLSEQVDGVMRIFGGVQOQLREIYKDNKNLFEVGENEPQKLVKFEVAGDIESLLDRKV 132
Qy 76 AVQNLVEAAEADLNHEFNEISLVD---YNSVLINERDE-KGNFVELGA-----EFL 124
Db 133 ALKRLADAENFOKARWQDNKEEDIVVYDAKADAELDDPESEDVERGSKASTLRLDFI 192
Qy 125 LESNAHFNLPVNTSSVOLPNVYNKDDPIINGVMSSEALNAVFNVENFQRPDPTLWQY 184
Db 193 EDN--FKN-KVNSYAAVQIPTDIYKGSTVILNELNWTALENVFMEENRQDPTLLWQV 249
Qy 185 FGSATGFRYIPGIKWTPBENGVIPTDCRNRGWYIOAATSPKDIVILVDVSGSMKGLRMT 244
Db 250 FGSATGTRYIPATPRAPK-IDLYDVRRRPMTIOGASSPKDMVIIVDVSGSVGLTLK 308
Qy 245 IAKHTITITLDTLGENDFVNIAYNDYVHYIEPCFGILVQADNRDREHFKLLVEELMVK 304
Db 309 LMKTSVCEMLDITLSDDDYNNVASFNEKAQPVSCPTH-LVQANVRNKKVFEKAVQGVAK 366
Qy 305 GVGVDQALREAPQILKQFOEAKQSGSLCNOAIMLISDGAVEDYEPVEKYNWDPCKVRVF 364
Db 367 GTTGKAGPEYAPDQLQNSNITRAN--CNKIMMFTDGGEDRVQDVFEKYNWENRTVRVF 424
Qy 365 TYLIGREVFSADRMKMIACNNKGYTYQISTLADTQENWMEYLHVLSPMVI--NHDHDI 422
Db 425 TFSVGQHYNDVTPLOMACANKGYFEIPISGAIRINTOEYLDVLRGPMVLAKGAKQV 484
Qy 423 WTEAYNMSKLLSQAQSLTLLTAVAMPVFS-----KKNETRSHGILLGVGSDVALR 474
Db 485 WTNVYED-----ALGLGLVVTGTLVFNLTODGPEKQKQ-----LILGVMGIDVALN 532
Qy 475 ELMKLAIRYKLVGHVAFYALNTNGYILSHPDRLPL---YREGKKLKPKNYSVDSEVE 531
Db 533 DIKRLTPTNTLGANGYVFAIDLNGYVLLHPLNPKPQTNNPREPVTL-----DFLDAE 583
Qy 532 WEDQ-ABSLRTAMINRETGTLSMDVKVPMKGRKRVFLTNDYFPTDTSDFPFLSGAVLSR 590
Db 584 LEDENKEIRSMIDGNKGKHQIRTLVKSLDERYIDEVTNRYTWPIRSTNYSGLVLP 643
Qy 591 GHGEYI-----LLGNTSVBEGUHLHPLDALAGOWIYICITIDDPHRK 634
Db 644 YSTFYQANLSDQILQVKYFEFLPSSFESEG-HVFIAPR-----EYC-KOLNASDNN 694
Qy 635 LSQLEAMIRFLTRKDPD-LECDEELVREVLFDVAVTAPM-EAYWTALALNMSESEHVVD 692
Db 695 TEFKXNFIELMEKVTPOSKOCNNFLNLHLLDGTITQQLVERVWRDQDLN-----TVSLL 749
Qy 693 MAFGLTRAGLRSSLFVSGSEKVSDRKFLTPDEASVFTLDRFPL--WYRQASEHPAGSF 749
Db 750 AVFAATDGGITR-----VFNKAEDWTENPEPNASFYRSLDN--HGY 792
Qy 750 VFN-----LRWAGP-ESAGEPMVVTASTAVAVTVDKRTAIAAAAGVQMKLEFLQKRF 801
Db 793 VFKPPHODALLR-----PLELNDTVGILVSTAVELSLGRRTLPRPAAVGVKLDLEAWAEKF 848
Qy 802 WAATROQSTVDGPTQSC-----EDSLDCFVIDNNGFILI SKRSR---ETGR 846
Db 849 KVLASNRTHQDQP--QKCGPNSHCEMDCVNNEDLLCVLIDGGFLVLSNQNHQDQVGR 906
Qy 847 FLGEVDGAVLTQLLSMGVFSQVMTYDQAMCKPSSHHSAAQP---LVSPISAPL----- 898
Db 907 FFEVDANLMLALYNNFSYTRKESYDQAACAPQPPGNLGAAPRGVFPVPTVAFLNLAW 966
Qy 899 -TATRWLLQELVFLLEWSVWGSWYDRG---ABAKSVFHHSHKHKKQDPLQPCDTETYPVF 954
Db 967 TSAAAWSLFQQLLYGL---IYHSWFQADPAEAGSPETRESSCVMKQ-----TQY--- 1013

QY 955 VYQPAIREA-NGIVEGCPCKVFWVQIIPNSNLLLVTD-PTCDCSIFPPVLQEAATEVKY 1012
DB 1014 -YGSVNASYNALIDCGNCSRLFAQLRTWNLFFVVAEPKLSQCEAGRLQKETHCPA 1072
QY 1013 NASVKCDRMSQKLRRRPDSCHAFHPEVRVEADRGWAGFSSPNPLCLGLCPCRCQ--EHIG 1070
DB 1073 DGPEQCELVQPRYRGPCHICFDYN----ATEDTSDCGRGASFPSPSLGLVLSQLLLLG 1128
QY 1071 MPNTPVPVLLGGNIRV 1087
DB 1129 LPPRPQPVLVHASRRL 1145
RESULT 14
US-09-397-550-20
; Sequence 20, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 1145
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-397-550-20
Query Match 20.7%; Score 1183.5; DB 4; Length 1145;
Best Local Similarity 29.6%; Pred. No. 3e-107;
Matches 343; Conservative 209; Mismatches 436; Indels 169; Gaps 42;
QY 16 WADTGGDLYNTVTKYSGSLLOKVKDVESLKIIEVDGLVLRKFSDEMNLARKV 75
DB 73 WARRLEQEVGDGVRIFGGVQQLREIYKDNRLFEVNEPEQKLVKAGDIESLLDRKKV 132
QY 76 AVQNLVEAAEADLNHFNESLFD---YNSVLINERDE-KGNFVELGA-----EFL 124
DB 133 ALKRLADAENFQKAHRWQDNKEEDIVVYDADAELDPEDSEDVERGSKASTLRDLFI 192
QY 125 LESNAHFNLPVNTSSVOLPTNVNKPDPDILNGVYMSEALNAVFNENFQRPDTLTWQY 184
DB 193 EDPN--FKN-KVNSYAAVQIPTDIYKGSTVILNLTWLEALNENFMRNRQDPTLLMQV 249
QY 185 FGSATGFRIYPIGKIWTPDENGVIITPCRNRGWYIOAATSPKDIVILVDVSGSMGLRMT 244
DB 250 FGSATGVTRYYPATPRAPK-IDLVDRRRPWIQASSPKDMVILVDVSGVSGLT 308
QY 245 IAKHTITLTDLTGENDFVNIIANDYVHYIEPCFKGILVQADRDNRHFKLVEBLMYK 304
DB 309 LMKTSVCEMLDTLSDDDYNNVASFNEKAQPV-S-CFTH-LVQANVRNKKVFKEAVQGVAK 366
QY 305 GUGVVDQALBEAQILKQFEAKQSGSLCNOAIMLSDGAVEDYEPFEKYNWPCVKRVF 364
DB 367 GTTYKAGFEYAFDQLQNSNITRAN--CNKIMMFTDGGEDRVQDYFEKYNWPNRTVRVF 424
QY 365 TYLIGEVSPADRMKVIACNNKGYTYTQISTLADTQENVMYELHVLGRPMVI--NHDHDI 422
DB 425 TFSVGQHYNDVTPLOWMACANKGYFEISGIRINTQYLDVLDVGRPMVLAKGAKQVQ 484
QY 423 WTBYNWSKLLSSQASLTLLTTVAMPVS-----KQNETRSHGILLGVVGSVALR 474
DB 485 WTNVYED-----ALGLGLVVTGTLPVFNLTQDGPGEKKQ-----LILGVNGIDVALN 532
QY 475 ELMKLAPRYKLVGHVAFALNTNGYITLSHPDLRPL---YREGKLPKPNKYNVDLSEVE 531
DB 533 DIKRLTNYTLGANGYVFAIDLNGYVLLHPNLKRPQTNTNREPVTL-----DFLDAE 583

QY 532 WEDO-AESLRTAMINRETGTLSDMDVKVPMDKGRVLFLLTNDYFETDISDTPFSLGAVLSR 590
DB 584 LEDENKEEIRRSMDGNKGHKQIRTLUVKSLDERYIDVETRTNVTWPIRSTNYSLGLVLP 643
QY 591 GHGEYI-----LLGNTSVBEGHLDLHLPDLALAGDWIYCIITDIDPHRK 634
DB 644 YSTFYLOANLSQILQVKYFEFLPSSFESEG-HVFIAPR-----EYC-KOLNASDNN 694
QY 635 LSQLEAMIRFLTRKDPD-LECDEELVREVLFDVAVTAPM-EAYWTALALNMSSESHVVD 692
DB 695 TBLKNFIBELMEKVTDPDSKOCNNFLHNLILDTGITQOQLVERVMRQDNL-----TYSLL 749
QY 693 MAPLGTAGLLRSSLFGSEKVSDDRKFLTPDEASVFTLDRFPL---WYRQASEHPAGSF 749
DB 750 AVFAATDGGITR-----VFPNKAEDWTENPEPPNASFYRRSLDN--HGY 792
QY 750 VFN-----LRWABGP-ESAGEPMVVTASTAVAVTVDKRTATAAAGVQMKLEFLQRF 801
DB 793 VFKPPHQDALLR-----PLELENDTVGILVSTAVELSLGRRTLRPAVVGVKLDLEAWAEKF 848
QY 802 WAATROCSTVDGPTYQSC-----EODLDCFVIDNNGFILLISKRSR---ETGR 846
DB 849 KVLASNRTHQDP--QKCGPNSHCEMDCVNNEDLLCVLIDGGFLVLSNQNHQMDQVGR 906
QY 847 FLGEVDGAVLTOLLSMGVFSQVTMYDQAMCKPSSHHSAAQ--LVSPISAF-----898
DB 907 FFEVDANLMLALYNNFSYTRKESYDYQAACAPQPPGNLGAAPRGVFPVTVADFLNLAW 966
QY 899 -TATRWLLQELVLFLEWSVWGSWYDRG---AEAKSVFHHSHKHKKODPLQPCDTPYVPF 954
DB 967 TGAAMSLFQQLLYGL---IYHSWFQADPAEAEGSPETRESSCVMKQ-----TQY---1013
QY 955 VYQPAIREA-NGIVEGCPCKVFWVQIIPNSNLLLVTD-PTCDCSIFPPVLQEAATEVKY 1012
DB 1014 -YGSVNASYNALIDCGNCSRLFAQLRTWNLFFVVAEPKLSQCEAGRLQKETHCPA 1072
QY 1013 NASVKCDRMSQKLRRRPDSCHAFHPEVRVEADRGWAGFSSPNPLCLGLCPCRCQ--EHIG 1070
DB 1073 DGPEQCELVQPRYRGPCHICFDYN----ATEDTSDCGRGASFPSPSLGLVLSQLLLLG 1128
QY 1071 MPNTPVPVLLGGNIRV 1087
DB 1129 LPPRPQPVLVHASRRL 1145
RESULT 15
US-09-397-550-6
; Sequence 6, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-397-550-6
Query Match 20.6%; Score 1179.5; DB 4; Length 1109;
Best Local Similarity 30.0%; Pred. No. 7e-107;
Matches 332; Conservative 202; Mismatches 408; Indels 163; Gaps 40;
QY 16 WADTGGDLYNTVTKYSGSLLOKVKDVESLKIIEVDGLVLRKFSDEMNLARKV 75
DB 73 WARRLEQEVGDGVRIFGGVQQLREIYKDNRLFEVNEPEQKLVKAGDIESLLDRKKV 132

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OM protein - protein search, using sw model

Run on: November 16, 2005, 03:22:59 ; Search time 175 Seconds
(without alignments)
2606.093 Million cell updates/sec

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Perfect score: 5726
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pcp.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pcp.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pcp.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pcp.*
 - 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pcp.*
 - 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pcp.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pcp.*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pcp.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pcp.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pcp.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp.*
 - 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pcp.*
 - 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pcp.*
 - 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pcp.*
 - 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pcp.*
 - 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pcp.*
 - 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pcp.*
 - 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pcp.*
 - 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5726	100.0	1090	10	US-09-833-222A-10
2	5726	100.0	1090	14	US-10-119-624-10
3	5385.5	94.1	1207	16	US-10-128-558-176
4	5234.5	91.4	1075	15	US-10-257-174-34
5	5230.5	91.3	1114	15	US-10-257-174-35
6	3808	66.5	1310	15	US-10-357-022-12
7	3422	59.8	1091	9	US-09-875-423-5
8	3422	59.8	1091	14	US-10-162-012-18
9	3422	59.8	1091	15	US-10-162-102-18
10	3419.5	59.7	1077	17	US-10-902-531-24
11	3416.5	59.7	1091	9	US-09-875-423-2
					Sequence 10, Appl
					Sequence 10, Appl
					Sequence 176, Appl
					Sequence 34, Appl
					Sequence 35, Appl
					Sequence 12, Appl
					Sequence 5, Appl
					Sequence 18, Appl
					Sequence 24, Appl
					Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-833-222A-10
; Sequence 10, Application US/09833222A
; Publication No. US20030166045A1
; GENERAL INFORMATION:
; APPLICANT: Codd, Ellen
; TITLE OF INVENTION: cDNA encoding the Calcium Channel Alpha2Delta-4 Subunit
; FILE REFERENCE: calcium channel alpha2delta-4 subunit
; CURRENT APPLICATION NUMBER: US/09/833,222A
; CURRENT FILING DATE: 2001-04-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1090
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-222A-10

Query Match 100.0%; Score 5726; DB 10; Length 1090;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1090; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAVALGTRRRDRVKLWADTFGGDLVNTVTKYSGSLLLQKKYKDVESLKIIEVDGLBLVR	60
Db	1	MAVALGTRRRDRVKLWADTFGGDLVNTVTKYSGSLLLQKKYKDVESLKIIEVDGLBLVR	60
Qy	61	KFSEDENMLRRKVEAVQNVLEAAEADLNHEFNESLVFDYVNSVLINERDEKGNFVELG	120
Db	61	KFSEDENMLRRKVEAVQNVLEAAEADLNHEFNESLVFDYVNSVLINERDEKGNFVELG	120
Qy	121	AEFLLESNAHFSNLPVNTSISVQLPTNVNPKDILLGVYMSALNAVVFENFQRPDTL	180
Db	121	AEFLLESNAHFSNLPVNTSISVQLPTNVNPKDILLGVYMSALNAVVFENFQRPDTL	180

Sequence 15, Appl
Sequence 15, Appl
Sequence 6, Appl
Sequence 12, Appl
Sequence 22, Appl
Sequence 4, Appl
Sequence 11, Appl
Sequence 10, Appl
Sequence 263, Appl
Sequence 9, Appl
Sequence 23, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 30666, A
Sequence 13494, A
Sequence 9117, Ap
Sequence 35, Appl
Sequence 3, Appl
Sequence 11, Appl
Sequence 6, Appl
Sequence 2, Appl
Sequence 4, Appl
Sequence 1799, Ap
Sequence 114, App
Sequence 20, Appl
Sequence 1, Appl
Sequence 33, Appl
Sequence 34, Appl
Sequence 32, Appl
Sequence 36, Appl
Sequence 6, Appl
Sequence 23, Appl

181 TWQYFGSATGFFRIYPGKWTDPDENGVIITFCRNRMWYIOAATSPKDIVILVDVSGSMKG 240
181 TWQYFGSATGFFRIYPGKWTDPDENGVIITFCRNRMWYIOAATSPKDIVILVDVSGSMKG 240
241 LRMTIAKHTTTILDTLGTENDFNVIIAIYNDVHYIEPCFKGILVQADRDNRHFKLLVEE 300
241 LRMTIAKHTTTILDTLGTENDFNVIIAIYNDVHYIEPCFKGILVQADRDNRHFKLLVEE 300
301 LMVKGVGVDOALREAFQILKQOEAKOGSICHOAINLISDGAVEDYEPVFEKYNPDCK 360
301 LMVKGVGVDOALREAFQILKQOEAKOGSICHOAINLISDGAVEDYEPVFEKYNPDCK 360
361 VRVFTYLI GREVSFADRMKWIACNNKGYTQISTLADTQENWMEYLHVLSPRPMVINHDH 420
361 VRVFTYLI GREVSFADRMKWIACNNKGYTQISTLADTQENWMEYLHVLSPRPMVINHDH 420
421 IIWTEAYMDSKLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSVALRELMLKLA 480
421 IIWTEAYMDSKLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSVALRELMLKLA 480
481 PRYKLGVHGAFINTNNGYILSHPDRLPLYREGKKLPKPNYNSVDLSEVWEDQAESLR 540
481 PRYKLGVHGAFINTNNGYILSHPDRLPLYREGKKLPKPNYNSVDLSEVWEDQAESLR 540
541 TAMINRETGTLSDMKVPMKDKGRVLFNTDIFFTDIDSPFSLGAVLSRGHGEYILLGN 600
541 TAMINRETGTLSDMKVPMKDKGRVLFNTDIFFTDIDSPFSLGAVLSRGHGEYILLGN 600
601 TSVEEGLHDLHPDLALAGDWIYICITDIDPHRKLSOLEAMIRFLTRKOPDLCEBELVR 660
601 TSVEEGLHDLHPDLALAGDWIYICITDIDPHRKLSOLEAMIRFLTRKOPDLCEBELVR 660
661 EVLFDVAVTAPMEAYWTALANMSESESHVVDMAFLGTRAGLLRSSLFVSGSEKVSORKEL 720
661 EVLFDVAVTAPMEAYWTALANMSESESHVVDMAFLGTRAGLLRSSLFVSGSEKVSORKEL 720
721 TPDEASVFTLDRFPLWYRQASEHPAGSFVFNLRWAEGPSAGEPMVVTASTAVAVTVDK 780
721 TPDEASVFTLDRFPLWYRQASEHPAGSFVFNLRWAEGPSAGEPMVVTASTAVAVTVDK 780
781 RTAIAAAAGVOMKLEFLORFKAATRCSTVDGPTYQSCEDSDLCFCFVIDNNGFILLISK 840
781 RTAIAAAAGVOMKLEFLORFKAATRCSTVDGPTYQSCEDSDLCFCFVIDNNGFILLISK 840
841 SRETGRFLGVDGAVLTOLLMSGVFSQVTMYDYQAMCKPSSHHSAAQPLVSPISAFITA 900
841 SRETGRFLGVDGAVLTOLLMSGVFSQVTMYDYQAMCKPSSHHSAAQPLVSPISAFITA 900
901 TRWLLQELVLFLEWSVWGSWYDRGAESKSVFHHSHKKQDPLQPCDTEYPVVTYQPAI 960
901 TRWLLQELVLFLEWSVWGSWYDRGAESKSVFHHSHKKQDPLQPCDTEYPVVTYQPAI 960
961 REANGIVECGPCQKVFVVOQIPNSNLLLVLTPTDCDSIPPPVLOBATEVKYNASVKCDR 1020
961 REANGIVECGPCQKVFVVOQIPNSNLLLVLTPTDCDSIPPPVLOBATEVKYNASVKCDR 1020
1021 MRSQKLRPRRSDSCHAFHPEVRVADRWAGFSSPNPLCLGLCPCROEHTGMPMNTVPVVL 1080
1021 MRSQKLRPRRSDSCHAFHPEVRVADRWAGFSSPNPLCLGLCPCROEHTGMPMNTVPVVL 1080
1081 LGGNIRVYAL 1090
1081 LGGNIRVYAL 1090

RESULT 2
US-10-119-624-10
; Sequence 10, Application US/10119624
; Publication No. US20030170785A1
; GENERAL INFORMATION:
; APPLICANT: Qin, Ning
; APPLICANT: Codd, Ellen

; TITLE OF INVENTION: cDNA Encoding a Human No. US20030170785A1el Alpha2 Delta4 Calcium
; FILE REFERENCES: ORT-1622
; CURRENT APPLICATION NUMBER: US/10/119,624
; CURRENT FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US 09/833,222
; PRIOR FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1090
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-119-624-10

Query Match 100.0%; Score 5726; DB 14; Length 1090;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1090; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAVALGTRRRDRVKLWADTFGGDLVNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLLEVR 60
DB 1 MAVALGTRRRDRVKLWADTFGGDLVNTVTKYSGSLLLQKKYKDVESSLKIEEVDGLLEVR 60
QY 61 KFSDEMNNMLRRKVEAVQNLVEAABEADLNHBFNESLVFDYNSVLINERDEKGNFVELG 120
DB 61 KFSDEMNNMLRRKVEAVQNLVEAABEADLNHBFNESLVFDYNSVLINERDEKGNFVELG 120
QY 121 APLLESNAHFSLNLPVNTSISSVOLPTVYNKDPDILNGVYMSEALNAVVENFQRDPTL 180
DB 121 APLLESNAHFSLNLPVNTSISSVOLPTVYNKDPDILNGVYMSEALNAVVENFQRDPTL 180
QY 181 TWQYFGSATGFFRIYPGKWTDPDENGVIITFCRNRMWYIOAATSPKDIVILVDVSGSMKG 240
DB 181 TWQYFGSATGFFRIYPGKWTDPDENGVIITFCRNRMWYIOAATSPKDIVILVDVSGSMKG 240
QY 241 LRMTIAKHTTTILDTLGTENDFNVIIAIYNDVHYIEPCFKGILVQADRDNRHFKLLVEE 300
DB 241 LRMTIAKHTTTILDTLGTENDFNVIIAIYNDVHYIEPCFKGILVQADRDNRHFKLLVEE 300
QY 301 LMVKGVGVDOALREAFQILKQOEAKOGSICHOAINLISDGAVEDYEPVFEKYNPDCK 360
DB 301 LMVKGVGVDOALREAFQILKQOEAKOGSICHOAINLISDGAVEDYEPVFEKYNPDCK 360
QY 361 VRVFTYLI GREVSFADRMKWIACNNKGYTQISTLADTQENWMEYLHVLSPRPMVINHDH 420
DB 361 VRVFTYLI GREVSFADRMKWIACNNKGYTQISTLADTQENWMEYLHVLSPRPMVINHDH 420
QY 421 IIWTEAYMDSKLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSVALRELMLKLA 480
DB 421 IIWTEAYMDSKLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSVALRELMLKLA 480
QY 481 PRYKLGVHGAFINTNNGYILSHPDRLPLYREGKKLPKPNYNSVDLSEVWEDQAESLR 540
DB 481 PRYKLGVHGAFINTNNGYILSHPDRLPLYREGKKLPKPNYNSVDLSEVWEDQAESLR 540
QY 541 TAMINRETGTLSDMKVPMKDKGRVLFNTDIFFTDIDSPFSLGAVLSRGHGEYILLGN 600
DB 541 TAMINRETGTLSDMKVPMKDKGRVLFNTDIFFTDIDSPFSLGAVLSRGHGEYILLGN 600
QY 601 TSVEEGLHDLHPDLALAGDWIYICITDIDPHRKLSOLEAMIRFLTRKOPDLCEBELVR 660
DB 601 TSVEEGLHDLHPDLALAGDWIYICITDIDPHRKLSOLEAMIRFLTRKOPDLCEBELVR 660
QY 661 EVLFDVAVTAPMEAYWTALANMSESESHVVDMAFLGTRAGLLRSSLFVSGSEKVSORKEL 720
DB 661 EVLFDVAVTAPMEAYWTALANMSESESHVVDMAFLGTRAGLLRSSLFVSGSEKVSORKEL 720
QY 721 TPDEASVFTLDRFPLWYRQASEHPAGSFVFNLRWAEGPSAGEPMVVTASTAVAVTVDK 780
DB 721 TPDEASVFTLDRFPLWYRQASEHPAGSFVFNLRWAEGPSAGEPMVVTASTAVAVTVDK 780
QY 781 RTAIAAAAGVOMKLEFLORFKAATRCSTVDGPTYQSCEDSDLCFCFVIDNNGFILLISK 840
DB 781 RTAIAAAAGVOMKLEFLORFKAATRCSTVDGPTYQSCEDSDLCFCFVIDNNGFILLISK 840

QY 841 SRETGRFLGVDGAVLTQLLSMGVFSQVTWYDYQAMCKPSSHHSAQAQPLVSPISAFITA 900
DB 841 SRETGRFLGVDGAVLTQLLSMGVFSQVTWYDYQAMCKPSSHHSAQAQPLVSPISAFITA 900
QY 901 TRWLLQELVLFLEWSVWGSYDRGAESVFFHSHKHKKODPLOCDDTEYPVYQPAI 960
DB 901 TRWLLQELVLFLEWSVWGSYDRGAESVFFHSHKHKKODPLOCDDTEYPVYQPAI 960
QY 961 REANGIVECCPCQKVQVVOQIPNSNLLLVTDPTCDCSIIPPVLQEAATEVKYNASVKCDR 1020
DB 961 REANGIVECCPCQKVQVVOQIPNSNLLLVTDPTCDCSIIPPVLQEAATEVKYNASVKCDR 1020
QY 1021 MRSQKLRRRPPDSCHAFHPEVRVADRGWAGFSSPNPLCLGLCPCRBQSHIGMPNTPVPVL 1080
DB 1021 MRSQKLRRRPPDSCHAFHPEVRVADRGWAGFSSPNPLCLGLCPCRBQSHIGMPNTPVPVL 1080
QY 1081 LGGNIRVYAL 1090
DB 1081 LGGNIRVYAL 1090

RESULT 3

US-10-128-558-176
; Sequence 176, Application US/10128558
; Publication No. US20040219521A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Gezhi
; APPLICANT: Boyle, Bryan J
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 812A
; CURRENT APPLICATION NUMBER: US/10/128,558
; CURRENT FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: US 60/339,453
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: Pt-FL_genes Version 6.0
; SEQ ID NO 176
; LENGTH: 1207
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-558-176
Query Match 94.1%; Score 5385.5; DB 16; Length 1207;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 1032; Conservative 6; Mismatches 13; Indels 3; Gaps 2;
QY 11 DRVKLWADTGGDLNTVTYKSGSLLOKKYKDVESLSKTEIEVDGLELVKRFKSEDNMNL 70
DB 145 ETVKLWADTGGDLNTVTYKSGSLLOKKYKDVESLSKTEIEVDGLELVKRFKSEDNMNL 204

QY 71 RRKVEAVQNLVEAAEADLNMHEFNESLVDYDYNVSLINERDEKGNFVELGAELLESNAH 130
DB 205 RRKVEAVQNLVEAAEADLNMHEFNESLVDYDYNVSLINERDEKGNFVELGAELLESNAH 264
QY 131 FSNLPVNTSSSVOLPTNPNYKDPDILNGVYMSSEALNAVVENFORDPTLTWQYFGSATG 190
DB 265 FSNLPVNTSSSVOLPTNPNYKDPDILNGVYMSSEALNAVVENFORDPTLTWQYFGSATG 324
QY 191 FFRYIPGIKWTPDENGVIPTDCRNRGWYIOAATS PKD I V I L V D V S G S M K G L R M T I A X H T I 250
DB 325 FFRYIPGIKWTPDENGVIPTDCRNRGWYIOAATS PKD I V I L V D V S G S M K G L R M T I A X H T I 384
QY 251 TTILDTLGENDFNIIAYNDYVHYI BPCFKGILVQADRDNRHFKLLVEELMVKGVGVVD 310
DB 385 TTILDTLGENDFNIIAYNDYVHYI BPCFKGILVQADRDNRHFKLLVEELMVKGVGVVD 444
QY 311 QALREAFQILKQFEAKQGLCNQAI ML I S D G A V E D Y E P F E K Y N N P D C K V R V T Y L I G R 370
DB 445 QALREAFQILKQFEAKQGLCNQAI ML I S D G A V E D Y E P F E K Y N N P D C K V R V T Y L I G R 504
QY 371 EVSFADRMKWIACNNKGYTQTISTLADTQENVMEYLHVL SRPMVINHDHDI I M T E A Y M D S 430
DB 505 EVSFADRMKWIACNNKGYTQTISTLADTQENVMEYLHVL SRPMVINHDHDI I M T E A Y M D S 564
QY 431 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSVALRELMLAPRYKLGVHG 490
DB 565 KLLSSQAQSLTLLTTVAMPVFSKKNETRSHGILLGVVGSVALRELMLAPRYKLGVHG 624
QY 491 AFLNTNNGYILSHPDRLPLYREGKCLKPKPNYSVDLSEVEDOAEBSLTAMINRETGT 550
DB 625 AFLNTNNGYILSHPDRLPLYREGKCLKPKPNYSVDLSEVEDOAEBSLTAMINRETGT 684
QY 551 LSMDVKVPMDKGRVLF LTNDYEF TDI S D T P F S L G A V L S R G H G E Y I L L G N T S V E E G L H D L 610
DB 685 LSMDVKVPMDKGRVLF LTNDYEF TDI S D T P F S L G V V L S R G H G E Y I L L G N T S V E E G L H D L 744
QY 611 LHPDLALAGDWIYCI TDI D P D H R K L S O L E A M I R F L T R K D P D L C D B E L V R E V L F D A V V T A 670
DB 745 LHPDLALAGDWIYCI TDI D P D H R K L S O L E A M I R F L T R K D P D L C D B E L V R E V L F D A V V T A 804
QY 671 PWEAYWTALANMSESEHVVDMAF L G T R A G L L R S S L F V G S E K V S D R K F L T P D E A S V F T 730
DB 805 PWEAYWTALANMSESEHVVDMAF L G T R A G L L R S S L F V G S E K V S D R K F L T P D E A S V F T 864
QY 731 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAGV 790
DB 865 LDRFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAGV 924
QY 791 QMKLEFLQKFWAATRCSTVDGPTQSCEDSDLD C F V I D N N G F I L I S K S R E T G R F L G E 850
DB 925 QMKLEFLQKFWAATRCSTVDGPTQSCEDSDLD C F V I D N N G F I L I S K S R E T G R F L G E 984
QY 851 VDGAVLTOLLSCMGVFSQVTWYDYQAMCKPSSHHSAQAQPLVSPISAPLTATRWLLQSELV 910
DB 985 VDGAVLTOLLSCMGVFSQVTWYDYQAMCKPSSHHSAQAQPLVSPISAPLTATRWLLQSELV 1044
QY 911 FLLEWSVWGSYDRGAESVFFHSHKHKKQDPLQPCDTEYPVYQPAIREANGIVECG 970
DB 1045 FLLEWSVWGSYDRGAESVFFHSHKHKKQDPLQPCDTEYPVYQPAIREANGIVECG 1104
QY 971 PCOKVFWVQOI P N S N L L L V T D P T C D C S I P P P V L Q E A T E V K Y N A S V K C D R M R S O K L R R R P 1030
DB 1105 PCOKVFWVQOI P N S N L L L V T D P T C D C S I P P P V L Q E A T E V K Y N A S V K C D R M R S O K L R R R P 1164
QY 1031 DSCHAFHPEVRVADRGWAGFSSPNP--LCLGLC 1062
DB 1165 DSCHAFHPEVRVADRGWAGFSSPNP--LCLGLC 1197

RESULT 4

US-10-257-174-34
; Sequence 34, Application US/10257174


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Qy 191 FFRIYPGKWTDPDENGVTFCRNGWYIOATSPKDIIVILVDVSGMKGLRMTIAKHTI 250
Db 238 FFRIYPGKWTDPDENGVTFCRNGWYIOATSPKDIIVILVDVSGMKGLRMTIAKHTI 297
Qy 251 TTILDTLGENDFVNIAYNDVHYIEPCFKGILVQADRDNRHFKLLVEELMWKGVGVWD 310
Db 298 TTILDTLGENDFINIAYNDVHYIEPCFKGILVQADRDNRHFKLLVEELMWKGVGVWD 357
Qy 311 QALREAFQILKQOEAQKQSLCNOAIMLISDGAVEDYEPPEKYNWDPCKVRVETYILGR 370
Db 358 QALREAFQILKQOEAQKQSLCNOAIMLISDGAVEDYEPPEKYNWDPCKVRVETYILGR 417
Qy 371 EVSFADRMKWTACNNKGYTTOISTLADTQENVMELVHLSPPMVINHDHDIITEAYMDS 430
Db 418 EVSFADRMKWTACNNKGYTTOISTLADTQENVMELVHLSPPMVINHDHDIITEAYMDS 477
Qy 431 KLLSSQAQSLTLTTVAMPVFSKKNRSHRSHGILLGVVGSVDVALRELKMLAPRYKLGHVGY 490
Db 478 KLLSSQAQSLTLTTVAMPVFSKKNRSHRSHGILLGVVGSVDVALRELKMLAPRYKLGHVGY 537
Qy 491 AFLTNNGYILSHPDRLPLVREGKKLPKPNYNSVDLSEVWEQOASLRTAMINRETGT 550
Db 538 AFLTNNGYILSHPDRLPLVREGKKLPKPNYNSVDLSEVWEQOASLRTAMINRETGT 597
Qy 551 LSMGVKVPMDKGRVFLFTNDYFTDIDTPPFLGAVLSRGHGEYIILGNTSVEEGLHDL 610
Db 598 LSMGVKVPMDKGRVFLFTNDYFTDIDTPPFLGAVLSRGHGEYIILGNTSVEEGLHDL 657
Qy 611 LHPDLALAGDWIYICITDIDPHRKLQLEAMIRFLTRKDPDCEDEELVREVLFDVVTA 670
Db 658 LHPDLALAGDWIYICITDIDPHRKLQLEAMIRFLTRKDPDCEDEELVREVLFDVVTA 717
Qy 671 PMEAYWTALALNMSESEHVVDMAFLTRAGLRSSLFVGVSEKVSDRKFLTPDEASVFT 730
Db 718 PMEAYWTALALNMSESEHVVDMAFLTRAGLRSSLFVGVSEKVSDRKFLTPDEASVFT 777
Qy 731 LDRPPLMYROASEHPAGSFVFNLRWAECPESAGPMVVTASTAVAVTVDKRTAIAAAGV 790
Db 778 LDRPPLMYROASEHPAGSFVFNLRWAECPESAGPMVVTASTAVAVTVDKRTAIAAAGV 837
Qy 791 QMKLEFLQRFWAATROCSVTGQYVTCSDSDLDCEFDVNNGFILISKRSRTGRFLGE 850
Db 838 QMKLEFLQRFWAATROCSVTGQYVTCSDSDLDCEFDVNNGFILISKRSRTGRFLGE 897
Qy 851 VDGAVLTQLLSMGVFSQVWYDYQAMCKPSHHSSAAQPLVSPISAFELTATRWLLQLBLVL 910
Db 898 VDGAVLTQLLSMGVFSQVWYDYQAMCKPSHHSSAAQPLVSPISAFELTATRWLLQLBLVL 957
Qy 911 FLLEWSVMSWYDRGAEKSVFHHSHKHKKQDPLQPCDTEYPVYQPAIREANGIVECG 970
Db 958 FLLEWSVMSWYDRGAEKSVFHHSHKHKKQDPLQPCDTEYPVYQPAIREANGIVECG 1010
Qy 971 PCQKVFVQQIIPNSNLLLLVTDP - CDCSITPPVQLQATEVKYNASVKCDRMSQKLRRR 1029
Db 1011 PCQKVFVQQIIPNSNLLLLVTDP - CDCSITPPVQLQATEVKYNASVKCDRMSQKLRRR 1070
Qy 1030 PDSCHAFPHVRVADRGWAGFSSPNP - -LCLGLC 1062
Db 1071 PDSCHAFPHBENAQ - DCGGASDTSASPLLLLLPVC 1104
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RESULT 6

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US-10-257-022-12
; Sequence 12, Application US/10257022
; Publication No. US20030211499A1
; GENERAL INFORMATION:
; APPLICANT: REDDY, Roopa
; APPLICANT: THORNTON, Michael
; APPLICANT: BOWEN, Mark L.
; APPLICANT: TANG, Y. Tom
; APPLICANT: KHAN, Farrah A.
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: GANDHI, Ameena R.
```

```
; APPLICANT: YAO, Monique G.
; APPLICANT: SANJANWALA, Madhusudan M.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: NGUYEN, Dannel B.
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: YUE, Henry
; APPLICANT: SEILHAMER, Jeffrey J.
; APPLICANT: WALIA, Narinder K.
; APPLICANT: LAL, Preeti
; APPLICANT: KEARNEY, Liam
; APPLICANT: WALSH, Roderick T.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: LU, Yan
; APPLICANT: GREENE, Barrie D.
; APPLICANT: RAUMANN, Brigitte B.
; APPLICANT: ARVIZU, Chandra S.
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PI-0067 USN
; CURRENT APPLICATION NUMBER: US/10/257,022
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: US01/11206
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/195,595
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/196,872
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/199,020
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/200,552
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/202,348
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/203,495
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PERL Program
; SEQ ID NO 12
; LENGTH: 1310
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7473443CDI
US-10-257-022-12
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Query Match 66.5%; Score 3808; DB 15; Length 1310;
Best Local Similarity 80.5%; Pred. No. 4.3e-300;
Matches 750; Conservative 4; Mismatches 14; Indels 164; Gaps 2;

Qy 11 DRVKLWADTFGGDLVNTVTYKSGSLLLQKKYKDVESLSKIEEVDGLVLRKFSDEMMML 70
Db 374 ETVKLWADTFGGDLVNTVTYKSGSLLLQKKYKDVESLSKIEEVDGLVLRKFSDEMMML 433
Qy 71 RRKVEAVQNLVEAAEADLNHFENESLV ----- 98
Db 434 RRKVEAVQNLVEAAEADLNHFENESLVBPFGVGVGMSVTQSGVGVGMSVTQSGVGV 493
Qy 99 ----- 98
Db 494 GVGMSTLTSQGVGVGMSVRSQSGVGVGMSVTQSGVGVGMSVTQSGVGVGMSVRQ 553
Qy 99 ----- 98
Db 554 SGVGVGVGMSVTQSGVGVGMSVRSQSGVGVGMSVTQSGVGVGMSVTQSGVGVGMSVRQ 613
Qy 99 -----FDYNSVLINERDEKGNFVELGABFLLESNAHPSNLPVNTSISVQLPTNV 149
Db 614 SVGLTRPPQFDYNSVLINERDEKGNFVELGABFLLESNAHPSNLPVNTSISVQLPTNV 673
Qy 150 YNKDPDILNGVYMSEALNAVFVENFORDPTLTWQYFGSATGFFRIYPGIKWTPDENGVI 209
Db 674 YNKDPDILNGVYMSEALNAVFVENFORDPTLTWQYFGSATGFFRIYPGIKWTPDENGVI 733
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Qy 210 PDCNRGWYQAAATSPKDIIVILVDVSSGMKGLRMTIAKHITTTTDLTDLGENDFNIIAYN 269
Db 734 FDCNRGWYIOAAATSPKDIIVILVDVSSGMKGLRMTIAKHITTTTDLTDLGENDFNIIAYN 793
Qy 270 DYVHIIEPCFNGIILVQADRDNRHFKLLVEELMWKGVGVVDOALREAFQILUKQFOEAKQG 329
Db 794 DYVHIIEPCFNGIILVQADRDNRHFKLLVEELMWKGVGVVDOALREAFQILUKQFOEAKQG 853
Qy 330 SLCNQAIMLISDGAVEDEYEPFEKYNNPDCVKRVFTYILIGREVSPADRMKMWIACNNKGY 389
Db 854 SLCNQAIMLISDGAVEDEYEPFEKYNNPDCVKRVFTYILIGREVSPADRMKMWIACNNKGY 913
Qy 390 TQISTLATQBNVMYELHVLISRPVMIINHDDIIWTEAYMDSKLLSSQAQSLTLLTTVAMP 449
Db 914 TQISTLATQBNVMYELHVLISRPVMIINHDDIIWTEAYMDSKLLSSQAQSLTLLTTVAMP 973
Qy 450 VFSKKNETRSHGILLGVGVSVALRELKMLAPRYKLVGHGYAFINTNNGYILSHPDRLPL 509
Db 974 VFSKKNETRSHGILLGVGVSVALRELKMLAPRYKLVGHGYAFINTNNGYILSHPDRLPL 1033
Qy 510 YREGKCLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGTLSDMDVKVPMDKGRVLFLT 569
Db 1034 YREGKCLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGTLSDMDVKVPMDKGRVLFLT 1093
Qy 570 NDYFFTDISDTPFSLGAVLSRGHGEYILLGNVTSVEEGLHDLHLHPDLALAGDWIYCIITDID 629
Db 1094 NDYFFTDISDTPFSLGVVLSRGHGEYILLGNVTSVEEGLHDLHLHPDLALAGDWIYCIITDID 1153
Qy 630 PDHRKLSOLEAMIRFLTRKOPDLECDDELVREVLFDVAVTAPMEAYWTALALNMSESEH 689
Db 1154 PDHRKLSOLEAMIRFLTRKOPDLECDDELVREVLFDVAVTAPMEAYWTALALNMSESEH 1213
Qy 690 VVDNAFLGTAGLRRSSLFVGSEKVSORKFLTLPDEASVFTLDRFPPLWYRQASEHPAGSF 749
Db 1214 VVDNAFLGTAGLRRSSLFVGSEKVSORKFLTLPDEASVFTLDRFPPLWYRQASEHPAGSF 1273
Qy 750 VFNLURWAEGPESAGEPMVVTASTAVAVTVDKR 781
Db 1274 VFNLURWAEGP--GRPSAKGLPPPLCQTILKR 1302

RESULT 7
US-09-875-423-5
; Sequence 5, Application US/09875423
; Patent No. US20020081657A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; TITLE OF INVENTION: 21784, A NOVEL HUMAN CALCIUM CHANNEL
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-059001
; CURRENT APPLICATION NUMBER: US/09/875,423
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1091
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-875-423-5

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Qy	133	NLPWNTSISSVQJQJPTNNVKNKDDPDLINGVYNSXALNAVFTVENFORDPTLTWQYFGSATGFF	192
Db	162	NLPVNIISLSQVQPTNNVKNKDDPAIVGVYNSXALNAVFTVENFORDPSLWQYFGSAKGF	221
Qy	193	RIYPGIKWTPDENGVLTIFDCRNKGWYIOAATS PKDITVLVDVSGSKMGLRMTAKHTIT	252
Db	222	RQYPGIKWPEDENGVLTAFDCRNKRKYIOAATS PKDVVILVDVSGSKMGLRMTAKQTVSS	281
Qy	253	ILDTLGENDEVNIIAYNDYVHYIETPCFKGLVQADRDNRHFHKLLEELMKVGGVVDQA	312
Db	282	ILDTLGDGDDFFNIIYNEELHYVEPCLNGTLVQADRTNRKEHFREHLDKLFAKIGMLDIA	341
Qy	313	LREAFQILKOFQSAKQSGSLCNQAIMLISDGAVEDYBPVFEKYNWPDCKRVFTYILGREV	372
Db	342	LNEAFNIIISDFNHTGOGSICSAIMLITDGAVDYDTIFAKYNWPDCKRVFTYILGREA	401
Qy	373	SFADRMKWIACNKNKYVTOISTLADTOENVMEYLHVLRSBMVNIHHDHIIWTWEAYWDSKL	432
Db	402	AFADNLKWMACANKGFTQISTLADQOENVMEYLHVLRSBPVJIDQHDVVMTTAYIDSTL	461
Qy	433	LSSQA-----QSLTLTLTTVAMPVFSKKNETRSHGILLGVGSDVALRELMLKAPRYKLGVH	488
Db	462	PQAKLADDOGLVMTTVAMPVFSKQNETRSKGLGVGVGTDPVKELLKTIIPYKLGIIH	521
Qy	489	GYAFLNTNNGYIILSHPDLRLPYREGKKLKPKNYNSVDLSEVEWEDQASLRTAMINRET	548
Db	522	GYAFATNNGYIILTHPELRLPYLEGKK-RRKPNYSSVDLSEVEWEDRDDVLRNAMYNRKT	580
Qy	549	GTLSMDVKVPMDKGKVLFTNDYFTDITSDTPFSLGAVLSRGHGVEYILLGNTSVEEGLH	608
Db	581	GKFSMEVKKTVDKGKVLVMTNDYYTIDIKGTPFSLGVALSRHGKYPFRGNVTIIEEGLH	640
Qy	609	DLLHPDLALAGDWIYICITDIDPHRKLISOLEAMIRFLTRKDPLECEDEELVREVLFDVV	668
Db	641	DLEHPDVLADWSYCNTOHLHPEHRHLSQLEAIKLYLKGKEPLQCKELIQEVLFDVV	700
Qy	669	TAPMEAYWTALANMGEBSHVVDMAFLGTRAGLLRSSJFVGEKYSVDRKFLTPEDASV	728
Db	701	SAPIEAYTISLANKSENSDKGEVAFGLGTRTGLSRINLFGVAEQLTNQDFLKAGDKENI	760
Qy	729	FTLDRPLWYROASEHPAGSFVENLAWGSPESAGEPMVVTASTAVAVTVDKETAATAAA	788
Db	761	FNADHPFLWYRAAEQIAGSFVSIIPFTG--TVNKSNNVTASTSLOLDERKSPVVAAV	818
Qy	789	GVQMKLEFLQKFEWAATROGCTVDGPTYTOSCEDSDLDVFNNDNGFILISKRSRRTGRFL	848
Db	819	GIQMKLEFFQKFEWTASRQCASLDGKCSISCDDETVNCYLIDNNGFILVSEDYQTQDFF	878
Qy	849	GEVDGAVLTOLLNGVFSQVTMYDYQAMCKPSHHHSAQPLVSPISAFLTATRWLLQEL	908
Db	879	GEVEGAVMNKLLTWGSPFKRITLYDYQAMCRANKESDSDAHGLLDPYKAFLSAAKMTWEL	938
Qy	909	VLLELWSVWGSWYDRGAEAKSVFPHSHKHKKQDPLQCDTEYVPVYQPAIREANGIVE	968
Db	939	VLFLVFENLC-SWWHSDMTAKA-----QKQLTLEPCDTEYPAFVSERTIKETTGNIA	990
Qy	969	CGPCQKVFVVOQJPNSSLNLLLVTDPTCDSCSIFPVLQEAETEYKYNASVKCDNRMSOKLRR	1028
Db	991	CEDCSKSFVIOQJPNSSLNMLVVDVSSCLCESVAPIWTWPIETRYNSSLKCRLLKAKQIRR	1050
Qy	1029	RPDSCHAFHPEVRVEADRGWAGFSS	1053
Db	1051	RPSCHGFTPE---ENARECGGASS	1072

RESULT 8
US-10-162-012-18
; Sequence 18, Application US/10162012
; Publication No. US20030051660A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, RORY A.J.
; APPLICANT: SIILOS-SANTIAGO, INMACULADA

; Sequence 15, Application US/10162102		Db	462	--PQAQKLTDDQGPVLMTTVAMPVFSKQNETRSKIGILLGVVGTDPVKELLKTIPKYLK	519
; GENERAL INFORMATION:		Qy	487	VHGAFALNTNNGYILSHPLDLRLYREGKLLKPKPNYSVDLSEVWEDQAEASLTAMNR	546
; APPLICANT: Curtis, Rory A.J.		Db	520	IHGAFALNTNNGYILTHPELRLLYEKGK-RRKNYSVDLSEVWEDRDDVLRNMMVR	578
; APPLICANT: Gu, Wei		Qy	547	ETGTLSDNVKVPMDKGRVLFNTDFFFTDISDTPPSLGAVALSRGHGEYILLGNSTVEEG	606
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS		Db	579	KTGKFSMEVKTVDKGRVLMVTNDYYTIDIKGTPPSLGAVALSRGHGEYIFRGNVTITEEG	638
; FILE REFERENCE: 10448-190001		Qy	607	LHDLHPDLALAGDWIYCIITDIDPHRKLSOLEAMIRFLTRKDPDLCEDBELREVLFDA	666
; CURRENT APPLICATION NUMBER: US/10/162,102		Db	639	LHDLHPDVLADSEWYCNCTDLHPEHRLSLEAIAKLYLKGKPELLOCDKELIQEVLFDA	698
; PRIOR FILING DATE: 2000-06-06		Qy	667	VVTAPMEAYMTALALNNSESEHVVDMAFLGTRAGLLRSLFVGSEKVSORKKFLTPEDEA	726
; PRIOR APPLICATION NUMBER: PCT/US01/18340		Db	699	VVSAPTEAYMTSLANKSENSDKGVEVAFGLTRGLSRINLFLVGAELTNQDFLKAGDKK	758
; PRIOR FILING DATE: 2000-06-05		Qy	727	SVETLDRFPLWYQASEHPAGSFVNLRWAEGPSAGEPMVVTASTAVATVTKRTAIAA	786
; PRIOR APPLICATION NUMBER: US 09/875,423		Db	759	NIFNADHFFLWYRRAAEQIPGSFVYSIPFSTGP--VNKSNVVTASTSIQLLDERKSPVA	816
; PRIOR FILING DATE: 2001-06-05		Qy	787	AAGVQMKLEFLQKFWAATRCQSTVDGPPYTQSCEDSDLDCCFVIDNNGFILISKRSRETGR	846
; PRIOR APPLICATION NUMBER: PCT/US01/18398		Db	817	AVGIQMKLEFFQKFWTASQCASLDGKCSISCDDETVCYLIDNNGFILVSEDTQTGD	876
; PRIOR FILING DATE: 2000-06-05		Qy	847	FLGEVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHSSAAQPLVSPISAFLTRMLLQ	906
; PRIOR APPLICATION NUMBER: PCT/US01/18247		Db	877	FFGEIEGAVNMKLLTMGSPKRIITLYDYQAMCRANKESSDGAHGLLDPYNAPLSAVKIMT	936
; PRIOR FILING DATE: 2000-08-22		Qy	907	ELVLFILLESVWGSWYDRGAEAKSVFHHSHKHKKQDPLOPCDTEYFVVPVQPAIREANGI	966
; Remaining Prior Application data removed - See File Wrapper or PALM.		Db	937	ELVLFILVEFNLCS--SMHSDMTAKA-----QKLTQLEPCDTEYFAPVSBERTIKETTGN	988
; NUMBER OF SEQ ID NOS: 48		Qy	967	VECGPCQKVPVQOIPNSNLLLVLTPTCDCSIFPPVLQBEATEVKYNASVKCDRMRSQKL	1026
; SOFTWARE: FastSeq for Windows Version 4.0		Db	989	IACEDCSKSFVIOQIPSSNLFMVVVDSSCLCESVAPITMAPIEIRYNESLKCELRKAKQI	1048
; SEQ ID NO 15		Qy	1027	RRRPDSCHAFHPE 1039	
; LENGTH: 1091		Db	1049	RRRPESCHGFHPE 1061	
; TYPE: PRT					
; ORGANISM: Homo sapiens					
US-10-162-102-15					
Query Match 59.7%; Score 3416.5; DB 15; Length 1091;					
Best Local Similarity 60.3%; Pred. No. 2,4e-268; Mismatches 203; Indels 19; Gaps 6;					
Matches 623; Conservative 188; Mismatches 203; Indels 19; Gaps 6;					
Qy	13	VKLWADTFGGDLVNTVTKYSGSLLQKXYKDVESLKIIEVDGLYELVKFSEDMENMLRR	72		
Db	42	VKLWASAFGGEIKSIAAKYSGSLLQKXYKDVESLKIIEVDGLYELVKFSEDMENMLRR	101		
Qy	73	KVEAVQNLVAAERADLNHFNESLVFDYVNSVLINERDEKGNFVGLGAEFLLESNAHFS	132		
Db	102	KSEAVRLVAAERADLNHFNESLVFDYVNSVLINERDEKGNFVGLGAEFLLESNAHFS	161		
Qy	133	NLPVNTSISVQLPNTVYKNDPDLNGVYMSALNAVVENFQDRDPTLTWQYFGSATGFF	192		
Db	162	NLPVNTSISVQLPNTVYKNDPDLNGVYMSALNAVVENFQDRDPTLTWQYFGSATGFF	221		
Qy	193	RIYPGIKWTPDENGVIITFCRNRGWYIQAATSPKDVILVDVSGSMKGLMTAKHTITT	252		
Db	222	RIYPGIKWTPDENGVIITFCRNRGWYIQAATSPKDVILVDVSGSMKGLMTAKHTITT	281		
Qy	253	ILDTLGENDFWIIATYNDVHYIETPCFKGILVQADRNREHFKLLVEELMVKGVVQDA	312		
Db	282	ILDTLGENDFWIIATYNDVHYIETPCFKGILVQADRNREHFKLLVEELMVKGVVQDA	341		
Qy	313	LREAFQILKFOEAKQSGCLNQALIMLISDGAVEDYEPVFEKYNWPCDKVRVFTYLIQREV	372		
Db	342	LREAFQILKFOEAKQSGCLNQALIMLISDGAVEDYEPVFEKYNWPCDKVRVFTYLIQREV	401		
Qy	373	SPADRMKVIACNKGYYTQISTLADTQENWMEYLHLVSRPWNINHDHDIITWTEAYMDSKL	432		
Db	402	AFADNLKWMACNKGYYTQISTLADTQENWMEYLHLVSRPWNINHDHDIITWTEAYMDSKL	461		
Qy	433	LSSQAQSLT-----LTTVAMPVFSKNETRSKIGILLGVVGTDPVKELLKTIPKYLK	486		

Query Match 59.6%; Score 3411; DB 17; Length 1091;
Best Local Similarity 59.6%; Pred. No. 6,8e-268;
Matches 623; Conservative 191; Mismatches 213; Indels 18; Gaps 6;


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Qy 13 VKLWADTFGGDLVNTVTYKSGSLLOKKYKDVESLSKIEEVDGLELVKRFSEDMENMLRR 72
Db 42 VKLWASAFGGEIKSIAAKYSGSLLQKKYKEYEKDVAIEIDGLQVLVKLAKNMEEMPHK 101
Qy 73 KVEAVQNLVEAAEADLNHEFNESLVDYVNSVLINERDEKGNFVGLGAELFLESNAHFS 132
Db 102 KSEAVRRLVEAAEABHLKHEFDADLOVEYFNAVLINERDKGNFLELKGFEFILAPNDHFN 161
Qy 133 NLPVNTSISVQLPTNVYKDPDILNGVYMSALNAVVENFORDPDLTWQYFGSAGTFF 192
Db 162 NLPVNISLSDVQVPTNMYNKDPAIVNGVYMSLNVKVFVDNFORDPSLIWQYFGSAGTFF 221
Qy 193 RIYPGKIWTPDENGVIITFCRNRGWYIOAATSPKDIIVLVDVSGSMGLRMTIAKHTITT 252
Db 222 ROYPGIKWEPDENGVIATFDCRNRKWIYIOAATSPKDVILVDVSGSMGLRLTIKAKQTVSS 281
Qy 253 ILDTLGENDFVNIITAYNDYVHYIPCPKGIILVQADRONRHEFKLLVBEELMVKGVVDDQA 312
Db 282 ILDTLGDGDDFNIIITYNELHYVEPCLNGTLVQADRTNKEHFEHLDKLFAKGIGMLDIA 341
Qy 313 LREAFOILKQFOEAKOGSLCNOAIMLISDGAVEDYEPVEKYNWPCCKVRFVFTYLGREV 372
Db 342 LNEAFNLSDFNHTGOGSICQAIMLITDGAVDYTIPIFAKYNWPKRVIRIFTYLGREA 401
Qy 373 SFADRMKWIACNNKGYIYTOISTLADTOENYMEYLHLSRPMVINHDHDIITWEAYMDSKL 432
Db 402 AFADNLKWMACANKGFFTOISTLADVQENWMEYLHLSRPKVIDQEHVVWTEAYIDSTL 461
Qy 433 LSSQA-----QSLTLLTTVAMPVFSKQNETRSHGILLGVGSDVALRELKMLAPRYKLGVH 488
Db 462 POAQKLADDQGLVMTTVAMPVFSKQNETRSKGILLGVGSDVVPVKELLKTIPIKYLGIH 521
Qy 489 GYAFLNTNNGVILSHPDRLPLRYREGKLPKPKPNVNSVDLSEWEDQAESLRMTAMINRET 548
Db 522 GYAPAITNNGIILTHPELRPLRYBEGKK-RRKNPYSSVDLSEWEDRDDVLRNANVRKT 580
Qy 549 GTLSMDVKVPMDKGRVLFITNDYFFTDISTPFLGAVLSRGHGEYIILGNTSVBEGHL 608
Db 581 GKFSMEVKTVDKGRVLMVNTDYYTIDKGAFFSLGVALSRGHGKYFFRGNVTIEBGLH 640
Qy 609 DLLHPDLALAGDWIYICITDIDPHRKLSQLEAMIRFLTRKDPDLCEDEULVREVLDAVV 668
Db 641 DLEHPDVSLSADEWSYCNVDLHPEHRLHSQLEAKLYLKKGEPQLQCCKELIQSVLFDVV 700
Qy 669 TAPMEAAYTALALNMSESHVVDMAFLGTRAGILRSSLFVSGEKYSDRKFLTPEDASV 728
Db 701 SAPIEAYTSLALNKSNSDKGEVAFGLTRTGLSRINLFGAEQLTNQDFLKARDKENI 760
Qy 729 FTLDREPLWYRQASEHPAGSFVFNLRWAEGPESAGPEMVYTASTAVATVDKRTAIAAAA 788
Db 761 FNADHPPLWYRRAAEQIPGSFVYSIPESTG--TVNKSNNVTASTSIQLLDERKSPVVAAV 818
Qy 789 GVOMKLEFLORKFWAATROCSVDGPTYQSCESDLDLCFVIDNNGFILISKREBRTGRFL 848
Db 819 GIQMKLEFFORKFWASRQASLDGKCSICDDETVCYLIDNNGFILVSEDTYOTGDFF 878
Qy 849 GEYDGAVLTOLLSGVFSOVMTDYQAMCKPSSHHSAAQPLVSPISAFIATATRWLLQEL 908
Db 879 GEVEGAVNKKLLTWGSKFRLITLDYQAMCRANKESDSAGLLDLPYKAFUSAAKWIVTEL 938
Qy 909 VLFLEWMSVMSGYDRGAESVFFHSHKHKKQDPLQPCDTEYVPFVYQPAIREANGIVE 968
Db 939 VLFLEVFNLCS-SSWHSDMTAKA-----QKLKQTLPEPCDTEYPAFVSERTIKETTGNIA 990
Qy 969 CGFCQKVFVVOQIPNSNILLVITDPTDCSIFPPVLOEATEVYKYNASVKCDRMRSQKLRR 1028
Db 991 CEDCSKSFVQQIPSSNLFMVVDDSSCLCSVAPITMAPIEIRYNESLKERLKAQKIRR 1050
Qy 1029 RPSCHAFHPVRVEADRGWAGFSS 1053
Db 1051 RPSCHGFHPE---ENARECGGASS 1072
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RESULT 15
US-10-902-531-12
; Sequence 12, Application US/10902531
; Publication No. US20050042659A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/10/902,531
; PRIOR FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: US/09/397,550
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 1065
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-902-531-12

Query Match 59.6%; Score 3410.5; DB 17; Length 1065;
Best Local Similarity 60.3%; Pred. No. 7.2e-268;
Matches 619; Conservative 188; Mismatches 207; Indels 13; Gaps 5;

Qy 13 VKLWADTFGGDLVNTVTYKSGSLLOKKYKDVESLSKIEEVDGLELVKRFSEDMENMLRR 72
Db 42 VKLWASAFGGEIKSIAAKYSGSLLQKKYKEYEKDVAIEIDGLQVLVKLAKNMEEMPHK 101
Qy 73 KVEAVQNLVEAAEADLNHEFNESLVDYVNSVLINERDEKGNFVGLGAELFLESNAHFS 132
Db 102 KSEAVRRLVEAAEABHLKHEFDADLOVEYFNAVLINERDKGNFLELKGFEFILAPNDHFN 161
Qy 133 NLPVNTSISVQLPTNVYKDPDILNGVYMSALNAVVENFORDPDLTWQYFGSAGTFF 192
Db 162 NLPVNISLSDVQVPTNMYNKDPAIVNGVYMSLNVKVFVDNFORDPSLIWQYFGSAGTFF 221
Qy 193 RIYPGKIWTPDENGVIITFCRNRGWYIOAATSPKDIIVLVDVSGSMGLRMTIAKHTITT 252
Db 222 ROYPGIKWEPDENGVIATFDCRNRKWIYIOAATSPKDVILVDVSGSMGLRLTIKAKQTVSS 281
Qy 253 ILDTLGENDFVNIITAYNDYVHYIPCPKGIILVQADRONRHEFKLLVBEELMVKGVVDDQA 312
Db 282 ILDTLGDGDDFNIIITYNELHYVEPCLNGTLVQADRTNKEHFEHLDKLFAKGIGMLDIA 341
Qy 313 LREAFOILKQFOEAKOGSICNOAIMLISDGAVEDYEPVEKYNWPCCKVRFVFTYLGREV 372
Db 342 LNEAFNLSDFNHTGOGSICQAIMLITDGAVDYTIPIFAKYNWPKRVIRIFTYLGREA 401
Qy 373 SFADRMKWIACNNKGYIYTOISTLADTOENYMEYLHLSRPMVINHDHDIITWEAYMDSKL 432
Db 402 AFADNLKWMACANKGFFTOISTLADVQENWMEYLHLSRPKVIDQEHVVWTEAYIDSTL 461
Qy 433 LSSQAQSLTLLTTVAMPVFSKQNETRSHGILLGVGSDVALRELKMLAPRYKLGVHGYAF 492
Db 462 TDDQGP--VLMITTVAMPVFSKQNETRSKGILLGVGSDVVPVKELLKTIPIKYLGIHGYAF 519
Qy 493 LNTNNGYILSHPDRLPLRYREGKLPKPKPNVNSVDLSEWEDQAESLRMTAMINRETGTL 552
Db 520 AITNNGYIILTHPELRLLYBEGKK-RRKNPYSSVDLSEWEDRDDVLRNANVRKTGKFS 578
Qy 553 MDVKYPMDKGRVLFITNDYFFTDISTPFLGAVLSRGHGEYIILGNTSVBEGHLDDLH 612
Db 579 MEVKKTVDKGRVLMVNTDYYTIDKGFPSLGVALSRGHGKYFFRGNVTIEBGLHDLH 638
Qy 613 PDALAGDWIYICITDIDPHRKLSQLEAMIRFLTRKDPDLCEDEULVREVLFDVAVTAP 672
Db 639 PDVSLADEWSYCNVDLHPEHRLHSQLEAKLYLKKGEPQLQCCKELIQSVLFDVAVSAPI 698
Qy 673 EAYWTALALNMSESHVVDMAFLGTRAGILRSSLFVSGEKYSDRKFLTPEDBASFTLD 732
Db 699 EAYWTSLALNKSNSDKGEVAFGLTRTGLSRINLFGAEQLTNQDFLKAGDKENIFNAD 758
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Qy		733	RPLWYRQAASEHPAGS	FVFNLRWAEGPESAGEPVVTASTAVATVDKRTAIAAAAGVQM	792
Dd		759	HFLWYRAAEQIPGSEVYIPISTGP-	-VNKSUVVTASTSIQLLDERSPVVAACVIOM	816
Qy		793	KLEFLQRKFAAATQCSTVDGPTYQTSCEDSDLCFVLDNNGFTILI	SKSRBTGRFLGEVD	852
Dd		817	KLEFFQRKFMTASRQCASLGDKCSISCDDETVCYLIDNNGFILVS	EDYTQTGDFFGEIE	876
Qy		853	GAVLTOLLSGVFSQVMTYDYQAMCKPSSHHHSAAPLVSPISAFITATRWLLQEJVLFL	912	
Dd		877	GAVNKLLTWGSFKRIITYDYQAMCRANKESSDGAHGLDPYNAPFSAVKWINTELVLF	936	
Qy		913	LEMSVGWSYDRGAEAKSVFHSHKHKKQDLPLOPCDTPEYFVVYQPAIREANGIVECGPC	972	
Dd		937	VEFNLC-SWWHSDWTAKA-----QKLKQTLPEPCDTEYPAFVSERTIKETTGNIACEDC	988	
Qy		973	QKVFPVVOQIINSNLLLLLVTDPTCCDSIFPPVLOBATEKYKNASVKCDRMRSOKLRRRPS	1032	
Dd		989	SKSFVIOQIPSSNLFMVVVDSSCLCESVAPIWTAPTEIRYNESLKLERLKAQKIRRRES	1048	
Qy		1033	CHAFHPE	1039	
Dd		1049	CHGFHPE	1055	

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Job time : 180 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 17, 2005, 03:21:06 ; Search time 1916 Seconds
(without alignments)
4704.647 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9794790 seqs, 4134909567 residues

Total number of hits satisfying chosen parameters: 19589580

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	5726	100.0	3486	17	US-10-119-624-9
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8	3421.5	59.8	3528	9	US-09-728-628-12
9	3421.5	59.8	3528	24	US-10-972-024-117
10	3416.5	59.7	3276	9	US-09-875-423-3
11	3416.5	59.7	3276	15	US-10-162-012-16
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45	1150.5	20.1	3186	22	US-10-902-531-1

ALIGNMENTS

RESULT 1

US-09-833-222A-9
; Sequence 9, Application US/09833222A
; Publication No. US20030166045A1
; GENERAL INFORMATION:
; APPLICANT: Qin, Ning
; APPLICANT: Codd, Ellen
; TITLE OF INVENTION: CDNA encoding the Calcium Channel Alpha2Delta-4 Subunit
; FILE REFERENCE: calcium channel alpha2delta-4 subunit
; CURRENT APPLICATION NUMBER: US/09/833,222A
; CURRENT FILING DATE: 2001-04-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9

[illegible]

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QY 681 LeuAsnMetSerGluGluSerGluHisValValAspMetAlaPheLeuGlyThrArgAla 700
DB 2230 CTCAACATGTCCGAGGAGTCTGAACACGTGTGGACATGGCTTCTCTGGGCACCCGGCT 2289
QY 701 GlyLeuLeuArgSerSerLeuPheValGlySerGluLysValSerAspArgLysPheLeu 720
DB 2290 GGCTCTCTGAAGACAGCTTGTCTGGGTCTCGAGAGGTCTCCGACAGAAAGTTCTCTG 2349
QY 721 ThrProGluAspGluAlaSerValPheThrLeuAspArgPheProLeuTyrPyrArgGln 740
DB 2350 ACACCTGAGGACGAGCGCGTGTTCACCTGGACCGCTTCGCGTGTGTATACCGCCAG 2409
QY 741 AlaSerGluHisProAlaGlySerPheValPheAsnLeuArgTrpAlaGluGlyProGlu 760
DB 2410 GCCTCAGAGCATCTGCTGGCAGCTTCGTCTTCAACCTCCGCTGGGAGAGGACCAAGAA 2469
QY 761 SerAlaGlyGluProMetValValThrAlaSerThrAlaValAlaValThrValAspLys 780
DB 2470 AGTCGGGTGAACCATGGTGGTGACGCAAGCACAGCTGTGGGTGACCGTGGACAG 2529
QY 781 ArgThrAlaIleAlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLys 800
DB 2530 AGGACAGCCATTGCTGCAGCGCGGGCGTCCAAATGAAGCTGGAATTCCTCCAGCGCAA 2589
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DB 2650 GACAGTGATCTGACTGCTTCGTCTCATCGAACACACGCGGTTCATTCTGATCTCAAGAGG 2709
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DB 2710 TCCCGAGAGACGGAGATTTCTGGGGAGGTGGATGCTGTCTCTGACCCAGCTGCTC 2769
QY 861 SerMetGlyValPheSerGlnValThrMetTyrAspTyrGlnAlaMetCysLysProSer 880
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QY 881 SerHisHisSerAlaAlaGlnProLeuValSerProIleSerAlaPheLeuThrAla 900
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QY 901 ThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLeuGluTrpSerValTrpGlySer 920
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QY 1001 ProProValLeuGlnGluAlaThrGluValLysTyrAsnAlaSerValLysCysAspArg 1020
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RESULT 2
US-10-119-624-9
; Sequence 9, Application US/10119624
; Publication No. US20030170785A1
; GENERAL INFORMATION:
; APPLICANT: Qin, Ning
; APPLICANT: Codd, Ellen
; TITLE OF INVENTION: cDNA Encoding a Human No. US20030170785A1el Alpha2 Delta4 Calcium
; FILE REFERENCE: ORT-1622
; CURRENT APPLICATION NUMBER: US/10/119,624
; CURRENT FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US 09/833,222
; PRIOR FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 9
; LENGTH: 3486
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-119-624-9

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Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

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DB 250 GGGCGGGAGCTGTATAACACTGTGACCAATACTCAGGCTCTCTCTTGTGCGAAGAAG 309
QY 41 TyrLysAspValGluSerSerLeuLysIleGluGluValAspGlyLeuGluLeuValArg 60
DB 310 TACAAGATGTGGAGTCCAGTCTGAAGATCGAGGAGTGGATGGCTTGGAGCTGGTGAGG 369
QY 61 LysPheSerGluAspMetGluAsnMetLeuArgArgLysValGluAlaValGlnAsnLeu 80
DB 370 AAGTTCTCAGAGACATGGAGAACATGCTCGGAGGAAAGTCGAGGCGTCCAGAAATCTG 429
QY 81 ValGluAlaAlaGluAlaAspLeuAsnHisGluPheAsnGluSerLeuValPheAsp 100
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QY 101 TyrTyrAsnSerValLeuIleAsnGluArgAspGluLysGlyAsnPheValGluLeuGly 120
DB 490 TATTACAACCTCGTCTCTGATCAACAGAGAGGAGGAGCAACTTCGTGGAGCTGGGC 549
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Db 2170 GAGGTGCTGTTTGGACGGTGTGACAGCCCGCATGGAAAGCCCTACTTGGGACAGCGTGGCC 2229
Qy 681 LeuAsnMetSerGluGluSerGluHisValValAspMetAlaPheLeuGlyThrArgAla 700
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Db 2290 GGCCTCTCTGAGAAGCAGCTTGTTCGTGGGCTCCGAGAAGGTCTCCGACAGGAAGTTCTTG 2349
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Qy 821 AspSerAspLeuAspCysPheValIleAspAsnAsnGlyPheIleLeuIleSerLysArg 840
Db 2650 GACAGTGATCTGGACTGTCTTCGTCATCGCAACAACAGGGGTTCATTCGTATCTCCAAAGG 2709
Qy 841 SerArgGluThrGlyArgPheLeuGlyValAspGlyValAlaValLeuThrGlnLeuLeu 860
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Qy 861 SerMetGlyValPheSerGlnValThrMetTyrAspTyrGlnAlaMetCysLysProSer 880
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Db 2830 AGTACACACACAGTGCAGGCCAGCCCTGGTCAGCCCAATTTCTGCCTTCTTGACGGCG 2889
Qy 901 ThrArgTrpLeuLeuGlnGluLeuValPheLeuLeuGluTrpSerValTrpGlySer 920
Db 2890 ACCAGGTGGTGTCTGCAGGAGCTGGTCTGTCTCTCTGCTGAGTGGAGTGTCTGGGGCTCC 2949
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Db 2950 TGGTACGACAGAGGGCGGAGGCGCAAAAGTGTCTTCCATCACTCCCAACAAACAAG 3009
Qy 941 GluAspProLeuGlnProCysAspThrGluTyrProValPheValTyrGlnProAlaIle 960
Db 3010 CAGGACCCGTGCAGCCCTGCGACACGAGTACCCCGTGTCTGTTACCGCCGCGCCATC 3069
Qy 961 ArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLysValPheValValGlnGln 980
Db 3070 CGGAGGCCAACGGGATCGTGGAGTGGGGCCCTGCCAGAGGTATTTGTGTGCAGCAG 3129
Qy 981 IleProAsnSerAsnLeuLeuValThrAspProThrCysAspCysSerIlePhe 1000
Db 3130 ATTCCCAACAGTAACCTCTCTCTCTGTCGACAGACCCCACTGTGACTGCAGCATCTTC 3189
Qy 1001 ProProValLeuGlnGluAlaThrGluValLysTyrAsnAlaSerValLysCysAspArg 1020
Db 3190 CCACCACTGTCTGCAGGAGGCGACAGAAAGTCAATATATATATGCTCTGTCAATGTGACCGG 3249
Qy 1021 MetArgSerGlnLysLeuArgArgProAspSerCysHisAlaPheHisProGluVal 1040
Db 3250 ATCGGCTCCAGAAAGTCCCGCGGCGACAGACTCTCTGCCACGCCCTTCCATCCAGAGGTG 3309
Qy 1041 ArgValGluAlaAspArgGlyTrpAlaGlyPheSerSerProAsnProLeuCysLeuGly 1060
Db 3310 CGGGTTGAGCGGATCGAGGGTGGGTGGATTTTTCATCCCAACCCCTCTGTGCTGGGT 3369
Qy 1061 LeuCysProCysArgGlnGluHisIleGlyMetProMetAsnThrProValProValLeu 1080
Db 3370 CTGTGCCCCCTGCAGACAGGAGCATATAGGGATGCCAATGAACACACCTGTGCTGTGCTT 3429
Qy 1081 LeuGlyGlyAsnIleArgValTyrAlaLeu 1090
Db 3430 CTCGGGGGAAACATTCGCGTTTATGCCCTG 3459

RESULT 3
US-10-128-558-52
; Sequence 52, Application US/10128558
; Publication No. US20040219521A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Gezhi
; APPLICANT: Boyle, Bryan J
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE OF INVENTION: Polypeptides
; FILE REFERENCE: 812A
; CURRENT FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: US/10/128,558
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: US 60/339,453
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
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; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: pt_FL_genes Version 6.0
; SEQ ID NO 52
; LENGTH: 4841
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(3689)
US-10-128-558-52

Alignment Scores:
Pred. No.: 0 Length: 4841
Score: 5385.50 Matches: 1034
Percent Similarity: 97.47% Conservative: 5
Best Local Similarity: 97.00% Mismatches: 27
Query Match: 94.05% Indels: 1
DB: 21 Gaps: 0

US-09-833-222A-10 (1-1090) x US-10-128-558-52 (1-4841)

Qy 11 AspArgValLysLeuTrpAlaAspThrPheGlyAspLeuTyrAsnThrValThrLys 30
Db 498 GAAACAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATACACTGTGACCAA 557
Qy 31 TyrSerGlySerLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
Db 558 TACTCAGGCTCTCTCTTGTCTGCAGAAAGTACAAAGATGTGAGTCCAGTCTCAAGATC 617
Qy 51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
Db 618 GAGGAGGTGGATGGCTTGGAGCTGGTGAGGAAGTCTCAGAGGACATGGAGAGACATCTG 677
Qy 71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn 90
Db 678 CGGAGAAAGTGCAGGCGGTCCAGAAATCTGGTGAAGCTGCCGAGGAGGCGGACCTGAAC 737
Qy 91 HisGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArg 110
Db 738 CACGAATTCAATGAATCCCTGGTGTTCGACTATTACAACTCGGCTCCTGTATCAACGAGAGG 797
Qy 111 AspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHis 130
Db 798 GACGAAAGGGCAACTCTCGTGGAGCTGGGCGCGGAGTTCCTCTGGAGTCCAATGCTCAC 857
Qy 131 PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr 150
Db 858 TTCAGCAACTGCCGCTGAACACCTCCATCAGCAGCGTGCAGCTGCCCAACGCTGAC 917
Qy 151 AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe 170
Db 918 AACAAAGACCCAGATATTTAAATGGAGTCTACATGTCTGAAGCCTTGAATGCTGCTTC 977
Qy 171 ValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGly 190
Db 978 GTGGAGAACTTCCAGAGAGACCCCAACGTTGACCTGGCAATATTTTGGCAGTGAACCTGGA 1037
Qy 191 PhePheArgIleTyrProGlyIleLysTyrTrpThrProAspGluAsnGlyValIleThrPhe 210
Db 1038 TTCTTCAGGATCTATCCAGGTATAAATGGACACCTGATGAGAAATGGAGTCAATCTTT 1097
Qy 211 AspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIle 230
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Db	1098	GACTGCCGAAACCGCGCTGGTACATTCATCAAGCTGTACTTCTCCCAAGGACATAGTGATT	1157
QY	231	LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle	250
Db	1158	TTGGTGGACGTGAGCGCGCAGTATGAAGGGCGTGGAGTACTATTGCAAGCACACCATC	1217
QY	251	ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyAsnAsp	270
Db	1218	ACCACCAATCTTGACACCCCTGGGGGAGATGACTTCAATTAATATCATAGGCTACATGAC	1277
QY	271	TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn	290
Db	1278	TACGTCCATTACATCGAGCCTTGTTTTAAAGGATCCTCGTCAGCGCGGACCGAGACAAT	1337
QY	291	ArgGluHisPheLysLeuLeuValGluLeuMetValLysGlyValGlyValValAsp	310
Db	1338	CGAGAGCATTTCAAACTGCTGGTGGAGGAGTTGATGGTCAAAAGGTGTGGGGTCTGGGAC	1397
QY	311	GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGlnAlaLysGlnGlySer	330
Db	1398	CAAGCCTGAGAGAGCCTTCCAGATCCTGGAAGCAGTTCCAAAGGCGCAAGCAAGGAGC	1457
QY	331	LeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal	350
Db	1458	CTCTGCAACCAGCGCCATCATGTCTCATCAGCGACGGCGCGTGGAGACTACGAGCCGGTG	1517
QY	351	PheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArg	370
Db	1518	TTTGAGAAGTATAACTGGCCAGACTGTGAAGTCCGAGTTTTCATCTACCTCATTTGGGAGA	1577
QY	371	GluValSerPheAlaAspArgMetLysTropIleAlaCysAsnAsnLysGlyTyrTyrThr	390
Db	1578	GAAGTGTCTTTGCTGACCCCATGAAGTGGATTGCAATGCACAAACAAGGCTACTACAG	1637
QY	391	GlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer	410
Db	1638	CAGATCTCAACGCTGGCGGACACCCAGGAGAACGTGATGAATACCTGCACGCTGCTCAGC	1697
QY	411	ArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSer	430
Db	1698	CGCCCCATGTGTATCAACACGACACGACGATCATCTGGACAGAGCCTACATGGGACAGC	1757
QY	431	LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuThrThrValAlaMetProVal	450
Db	1758	AAGCTCTCAGCTCGCAGGCTCAGAGCCTGACACTGCTCACCCTGTGGCCATGCCAGTC	1817
QY	451	PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp	470
Db	1818	TTCAGCAAGAAGAAACGAAACCGCATCCCATGGCATTCCTCTGGGTGTGGTGGGCTCAGAT	1877
QY	471	ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr	490
Db	1878	GTGGCCCTGAGAGAGCTGATGAAGCTGGCGCCCCGTACAAAGCTTGGAGTGCAACGGATAC	1937
QY	491	AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr	510
Db	1938	GCCTTTCTGNACACCAACAATGGCTACATCTCTCCATCCCGACCTCGGCCCTCTGTAC	1997
QY	511	ArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal	530
Db	1998	AGAGAGGGGAAGAAACTAAACCCAAACCTTAACACACAGTGTGGATCTCTCCGAAGTG	2057
QY	531	GluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr	550
Db	2058	GAGTGGGAAGACAGAGCTGAATCTCTGAGAACAGCCATGATCAATAGGGAACAGGTACT	2117
QY	551	LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn	570
Db	2118	CTCTCCATGGATGTGAAGTTCCGATGGATTAAGGAGAGCGAGTTCTTTCTCTGACCAAT	2177
QY	571	AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg	590

Db	2178	GACTACTTCTTCACGGACATCAGCAGACCCCTTTTCAGTTTGGGGGTGGTGTCTCCCGG	2237
QY	591	GlyHisGlyGluTyrIleLeuLeuGlyAenThrSerValGluGluGlyLeuHisAspLeu	610
Db	2238	GGCCACGGAGAAATACATCTTCTGGGGAAACACGCTCTGTGGAAAGAGCCCTGCATGACTTG	2297
QY	611	LeuHisProAspLeuAlaLeuAlaGlyAspTyrIleTyrCysIleThrAspIleAspPro	630
Db	2298	CTTCACCCAGACCTGGCCCTGGCCGCTGACTGGATCTACTGCATCACAGATATTGACCCA	2357
QY	631	AspHisArgGlyLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro	650
Db	2358	GACCACCGGAAGCTCAGCCAGCTAGAGGCAATGATCCGCTTCTCACCAGAAAGGACCCA	2417
QY	651	AspLeuGluCysAspGluLeuValArgGluValLeuPheAspAlaValValThrAla	670
Db	2418	GACCTGGAGTGTGACAGAGAGCTGGTCCGGGAGGTGCTGTTTGACCGGTGGTGAGAGCC	2477
QY	671	ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisVal	690
Db	2478	CCCATGGAAGCCTACTGGACAGCGCTGGCCCTCAACATGTCCGAGGAGTCTGAACAGTG	2537
QY	691	ValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGly	710
Db	2538	GTGGACATGGCCTTCTGGGGCACCCGGGCTGGCTCTCTGAGAAGCAGCTTGTTCGTGGGC	2597
QY	711	SerGluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThr	730
Db	2598	TCCGAGAAGGTCTCCACAGGAAGTTCTTGACACCTTGAGGACAGGCCAGCGTGTCCACC	2657
QY	731	LeuAspArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheVal	750
Db	2658	CTGGACCGCTTCCCGCTGTGTACCCGCCAGGCTCTAGAGCATCTCTGCTGGCAGTTCGTC	2717
QY	751	PheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAla	770
Db	2718	TTCAACCTCCGCTGGCGAGAGGACAGAAAGTGGGGTGAACCCCATGTGTGTGACGGCA	2777
QY	771	SerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaGlyVal	790
Db	2778	AGCACAGCTGTGGCGGTGACCTGGACAAGAGACAGCCATTGCTGCAGCGCGGGCGTC	2837
QY	791	GlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThr	810
Db	2838	CAATGAAGCTGGAATTCCTCCAGCGCAATTCCTGGCGGCAACCGCGGAGTGCAGACT	2897
QY	811	ValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAsp	830
Db	2898	GTGGATGGGCGCTGCACACAGAGCTCGAGGACAGTGATCTGCATCTGCTCATCGAC	2957
QY	831	AsnAsnGlyPheIleuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGlu	850
Db	2958	AACAACGGGTTCATTCTGATCTCCAAGAGTCCCAGAGACGGGAAGATTTCTGGGGGAG	3017
QY	851	ValAspGlyValAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMet	870
Db	3018	GTGGATGGTGTCTCTGCACCCAGCTGCTCAGCATGGGGGTGTTACAGCAAGTACTATG	3077
QY	871	TyrAspTyrGlnAlaMetCysLysProSerSerHisHisSerAlaAlaGlnProLeu	890
Db	3078	TATGACTATCAGGCCATGTGCAAAACCTCGAGTCCACACACAGTGCAGCCGCCCTG	3137
QY	891	ValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeu	910
Db	3138	GTACGCCCAATTTCTGCCCTTTTGACGGCGAACAGGTGGCTGCTGCAGAGAGTGTGTCTG	3197
QY	911	PheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSer	930
Db	3198	TTCTCTGCTGGAGTGTCTGGGCTCTCTGGTACGACAGAGGGGCCGAGGCCAAAAGT	3257
QY	931	ValPheHisHisSerHisLysLysGlnAspProLeuGlnProCysAspThrGlu	950
Db	3258	GTCTTCCATCACTCCCAACAACACAAGAAGCAGGACCCCGCTGCAGCCCTGCCGACGGAG	3317

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Qy 951 TyrProValPheValTyrGlnProAlaIleArgGluAlaAenGlyIleValGluCysGly 970
Db 3318 TACCCCGTGTTCGTGTACAGCGGCCATCCGGAGGCCAACGGGATCGTGGAGTGGCGG 3377
Qy 971 ProCysGlnLysValPheValValGlnGlnIleProAenSerAenLeuLeuVal 990
Db 3378 CCCTGCCAAGAGGTATTTGTGGTCAGCAGATTCCTCCAAACAGTAACCTCTCTCTCTG 3437
Qy 991 ThrAapProThrCysAapCysSerIlePheProValLeuGlnGluAlaThrGluVal 1010
Db 3438 ACAGACCCCACTGTGACTGAGCATCTTCCACCACTGCTGCAGAGGCCACAGAGTGC 3497
Qy 1011 LysTyrAenAlaSerValLysCysAapArgMetArgSerGlnLysLeuArgArgPro 1030
Db 3498 AAATAATAATGCTCTGTCAAAATGTGACCGGATGGCTCCCAAGAGCTCCGCGCGACCA 3557
Qy 1031 AspSerCysHisAlaPheHisProGluValArgValGluAlaAapArgGlyTrpAlaGly 1050
Db 3558 GACTCTGCGCCAGCGCTTCCATCCAGAGGAGAAATGCCAGGACTCGCGCGCGCTCGGAC 3617
Qy 1051 PheSerSerProAenProLeuCysLeuGlyLeuCysProCysArgGlnGluHisIleGly 1070
Db 3618 ACCTGAGCTCGCGCCCTACTCTGCT-CCCTGTGTGTGCTTGGGGGCTACTGCCCCA 3676
Qy 1071 MetProMetAenThrPro 1076
Db 3677 ACTCTGCGGTGACACCA 3694

RESULT 4
US-10-257-174-10
; Sequence 10, Application US/10257174
; Publication No. US20040034194A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50022
; CURRENT APPLICATION NUMBER: US/10/257,174
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: PCT/US01/11797
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/196,603
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/199,417
; PRIOR FILING DATE: 2000-04-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 3228
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-257-174-10

Alignment Scores:
Pred No.: 0 Length: 3228
Score: 5234.50 Matches: 1013
Percent Similarity: 95.68% Conservative: 7
Best Local Similarity: 95.03% Mismatches: 34
Query Match: 91.42% Indels: 13
DB: 19 Gaps: 3

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Qy 12 ArgValLysLeuTrpAlaAapThrPheGlyGlyAapLeuTyrAenThrValThrLysTyr 31
Db 58 AGAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATACACTGTGACCAATAC 117
Qy 32 SerGlySerLeuLeuGlnLysLysTyrLysAapValGluSerSerLeuLysIleGlu 51
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Db 118 TCAGGCTCTCTTTGTGTCAGAAAGTACAAAGATGTGGAGTCCAGTCTCAAGATCGAG 177
Qy 52 GluValAapGlyLeuGluLeuValArgLysPheSerGluAapMetGluAenMetLeuArg 71
Db 178 GAGGTGATGGCTTGGAGCTGGTGAGGAGTTCTCAGAGGACATGGAGAAACATGCTGGCG 237
Qy 72 ArgLysValGluAlaValGlnAenLeuValGluAlaAaGluGluAlaAapLeuAenHis 91
Db 238 AGGAAAGTCGAGGCGGTCCAGAAATCTGTGTGAAGCTGCCGAGGAGGCGGACCTGAACAC 297
Qy 92 GluPheAenGluSerLeuValPheAapTyrTyrAenSerValLeuIleAenGluAap 111
Db 298 GAATTCATGAATCCCTGGTGTTCGACTATTACAACTCGGTCTGTATCAACAGAGGAC 357
Qy 112 GluLysGlyAenPheValGluLeuGlyValaGluPheLeuLeuGluSerAenAlaHisPhe 131
Db 358 GAGAAAGGCAACTTTCGTGGAGCTGGCGCGGAGTTCTCTCTGGAGTCCAATGCTCACATTC 417
Qy 132 SerAenLeuProValAenThrSerIleSerSerValGlnLeuProThrAenValTyrAen 151
Db 418 AGCAACCTGCGGTGAACACCTCCATCAGCAGCGTGCAGCTGCCACCACTGTATCAAC 477
Qy 152 LysAapProAapIleLeuAenGlyValTyrMetSerGluAlaLeuAenAlaValPheVal 171
Db 478 AAAGACCCAGATATTTAAATGGAGTCTACATGTCTGAAGCCTTGAATGCTGTCTCTGTG 537
Qy 172 GluAenPheGlnArgAapProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhe 191
Db 538 GAGAACTTCCAGAGAGACCCCAACGTTGACCTGGCAATATTTTGGCAGTGCACATGGAATTC 597
Qy 192 PheArgIleTyrProGlyIleLysTyrThrProAapGluAenGlyValIleThrPheAap 211
Db 598 TTCAGGATCTATCCAGGTATAAAATGGACACCTCATGAGAATGGAGTCAATTTACTTTTGC 657
Qy 212 CysAapAenArgGlyTrpTyrIleGlnAlaAaThrSerProLysAapIleValIleLeu 231
Db 658 TGGCGAAACCGCGCTGTGTACATTCAGCTGTCTACTTCTCCAAAGGACATAGTGAATTTG 717
Qy 232 ValAapValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThr 251
Db 718 GTGGAGTGAAGCGGACGATGAAGGGGCTGAGGATGACTATTGCCAAGCACCATCACC 777
Qy 252 ThrIleLeuAapThrLeuGlyGluAenAapPheValAenIleIleAlaTyrAenAapTyr 271
Db 778 ACCATCTTGGACACCTTGGGGGAGATGACTTCAATTAATCATAGGCTACATGACTAC 837
Qy 272 ValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAapAaGluAapAenArg 291
Db 838 GTCCATTACATCGAGCCTTGTTTTAAAGGATCTCTGTCCAGGCGGACCCGAGACATCGA 897
Qy 292 GluHisPheLysLeuLeuValGluLeuMetValLysGlyValGlyValValAapGln 311
Db 898 GAGCATTTCAAACTGCTGGTGGAGGAGTTGATGTCAAGAGGTGTGGGGGCTCGTGGACCA 957
Qy 312 AlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGlnAlaLysGlnGlySerLeu 331
Db 958 GCCCTGAGAGAAGCCTTCCAGATCTTCAAGCAGTTCCAAAGGCGCAAGGAGGAGCTC 1017
Qy 332 CysAenGlnAlaIleMetLeuIleSerAapGlyValaValGluAapTyrGluProValPhe 351
Db 1018 TGCAACCCAGGCCCATCTGCTCATCAGGCGCGGCCCTGGAGGACTACGAGCCCGGTGTTT 1077
Qy 352 GluLysTyrAenTrpProAapCysLysValArgValPheThrTyrLeuIleGlyArgGlu 371
Db 1078 GAGAGTATAACTGGCCAGACTGTAAAGTCCGAGTTTTCCTTACCTCATTTGGGAGAGAA 1137
Qy 372 ValSerPheAlaAapArgMetLysTyrIleAlaCysAenAenLysGlyTyrTyrThrGln 391
Db 1138 GTGTCTTTTCTGACCGCATGAAGTGGATTGTCATGCAACCAACAAAGGCTACTACACGAG 1197
Qy 392 IleSerThrLeuAlaAapThrGlnGluAenValMetGluTyrLeuHisValLeuSerArg 411
Db 1198 ATCTCAACGCTGGCGGACACCCAGGAGAACGTGATGGAATACCTGCACTGCTCAGCGCG 1257
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412 ProMetValIleAenHisAspHisAspIleIleTrpThrGluAlaTyrrMetAspSerLys 431
Db 1258 CCATGGTTCATCAACACGACCGACGATCATCTGGACAGAGGCCCTACATGGACAGCAAG 1317
Qy 432 LeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProValPhe 451
Db 1318 CTCCTCAGCTCGCAGGCTCAGAGCTGACACTGCTCACCACCTGTGGCCATGCCAGTCTTC 1377
Qy 452 SerLysIleAenGlnThrArgSerHisGlyIleLeuLeuGlyValValGlySerAspVal 471
Db 1378 AGCAAGAAGAACCAACCGCATCCCATGGCATTTCTCTGGGTGTGGTGGCTCAGATGTG 1437
Qy 472 AlaLeuArgGlnLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyrAla 491
Db 1438 GCCTTGAGAGGCTGATGAAGCTGGGCCCGCGGTACAGCTTGAGGTGCACGATAGGCC 1497
Qy 492 PheLeuAsnThrAenAenGlyTyrIleLeuSerHisProAspLeuArgProLeuTyrArg 511
Db 1498 TTTCTGAACACCAACATGCTACATCTCTCCATCCCGACCTCCGGGCCCTGTACAGA 1557
Qy 512 GluGlyLysLysLysProLysProAsnTyrAsnSerValAspLeuSerGluValGlu 531
Db 1558 GAGGGGAAGAACTAAACCCAAACCTTAACACAGAGTGGATCTCTCCGAAGTGGAG 1617
Qy 532 TrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThrLeu 551
Db 1618 TGGGAAGACCGGCTGNAATCTCTGAGAACAGCCATGATCAATAGGGAACAGGTACTCTC 1677
Qy 552 SerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsnAsp 571
Db 1678 TCGATGGATGTGAAGGTTCGATGGATAAAGGAAGCGAGTCTTTTCTCTGACCAATGAC 1737
Qy 572 TyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArgGly 591
Db 1738 TACTTCTTTCAGGACATCAGCGACACCCCTTTCAGTTTGGGGGTGGTGTCTCCCGGGC 1797
Qy 592 HisGlyGluTyrIleLeuLeuGlyAenThrSerValGluGluGlyLeuHisAspLeuLeu 611
Db 1798 CACGGAGATACATCTCTTCTGGGGAACACGCTGTGGGAAGAGCCCTGCATGACTTGCCT 1857
Qy 612 HisProAspLeuAlaLeuAlaGlyAspTyrPheTyrCysIleThrAspIleAspProAsp 631
Db 1858 CACCCAGACCTGGCCCTGGCCGGTGAAGTCTGATCTACTGCATCACAGATATTGACCCAGAC 1917
Qy 632 HisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspProAsp 651
Db 1918 CACCGGAAGCTCAGCCAGCTAGAGGCCATGATCCGCTTCTCACCAGGAAGGCCAGAC 1977
Qy 652 LeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAlaPro 671
Db 1978 CTGGAGTGTGACAGGAGCTGGTCCGGAGGTGCTGTTTGACCGGTGTGACAGCCCCC 2037
Qy 672 MetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisValVal 691
Db 2038 ATGGAAGCCTACTGGACAGCGCTGGCCCTCAACATGTCCGAGGAGTCTGAACAGTGGTG 2097
Qy 692 AspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGlySer 711
Db 2098 GACATGGCCCTTCCTGGGACCCCGGCTGGCTCTCTGAGAGCAGCTTGTTCGTGGGCTCC 2157
Qy 712 GluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeu 731
Db 2158 GAGAAGGTCTCCGACAGGAAGTTCCTGACACCTGAGGACGAGGCCAGCGTTCACCCCTG 2217
Qy 732 AspArgPheProLeuTyrTrpThrArgGlnAlaSerGluHisProAlaGlySerPheValPhe 751
Db 2218 GACCGCTTCCCGCTGTGTGTTACCGCAGCGCTCAGAGCATCTCTGCTGGCAGCTTCGCTTC 2277
Qy 752 AsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAlaSer 771
Db 2278 AACCTCGCTGGGACGAAGACCAAGAAAGTGGCGGTGAACCCCATGTGGTGGACGGCAAGC 2337

772 ThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaAlaGlyValGln 791
Db 2338 ACAGCTGTGGCGGTGACCGTGGACAGAGGACAGCCATTGCTGCAGCCCGGGCGTCCAA 2397
Qy 792 MetLysLeuGluPheLeuGlnArgLysPheTrpAlaIleThrArgGlnCysSerThrVal 811
Db 2398 ATGAAGCTGGAATTCCTCCAGCGCAAAATCTGGCGGCAACGCGGAGTGCAGCACTGTG 2457
Qy 812 AspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAspAen 831
Db 2458 GATGGGCCGTGCACACAGAGCTCGGAGGACAGTGATCTGGACTGCTTCATCGACAAC 2517
Qy 832 AsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGluVal 851
Db 2518 AACGGGTTTCATCTGATCTCCAAGAGTCCCAGAGAGCGGAAGATTTCTGGGGGAGGTG 2577
Qy 852 AspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMetTyr 871
Db 2578 GATGGTGTCTGCTGACCCAGCTGCTCAGACTGGGGGTGTTCAAGCAAGTACTATGTAT 2637
Qy 872 AspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAlaAlaGlnProLeuVal 891
Db 2638 GACTATCAGCCATGTGCAACCCCTCGAGTCACCAACAGTCAGCCAGCCCTTGCTC 2697
Qy 892 SerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluValLeuPhe 911
Db 2698 AGCCCAATTTCTGCCTTCTTGACGGCGCACCGAGTGGCTGTCAGAGCTGGTGTCTTC 2757
Qy 912 LeuLeuGluTyrTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSerVal 931
Db 2758 CTGCTGGAGTGAGTGTCTGGGGCTCTGTTACGACAGAGGGGCCGAGGCC----- 2808
Qy 932 PheHisHisSerHisHisHisLysLysGlnAspProLeuGlnProCysAspThrGluTyr 951
Db 2809 -----CACAAACACAGAAAGCAGGAGCCCTCGAGCCCTGCCACACGAGTAC 2856
Qy 952 ProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGlyPro 971
Db 2857 CCGGTGTTCTGTGTACCAGCGGCCATCCGGGAGGCCAACGGGATCGTGAGTGGCGGCC 2916
Qy 972 CysGlnLysValPheValValGlnGlnIleProAenSerAsnLeuLeuLeuValThr 991
Db 2917 TGCCAGAGGTATTTGTGTGCAGCAGATTCACCAACAGTAACCTCTCTCTCTGGTGACA 2976
Qy 992 AspProThr---CysAspCysSerIlePheProValLeuGlnGluAlaThrGluVal 1010
Db 2977 GACCCACCTTCTGCAGAAATGGGCTCCGGTCTCTGAGATATTGACCTTAACAGTGGCTTCT 3036
Qy 1011 LysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArgPro 1030
Db 3037 GCACATAATGCTCTGTCAAAATGTGACCGGATGCGCTCCAGAACTCCGCGGCGACCA 3096
Qy 1031 AspSerCysHisAlaPheHisProGluValArgValGluAlaAspArgGlyTrpAlaGly 1050
Db 3097 GACTCTGTCAGCCCTTCCATCCAGAGGAATGCCAGGACTGCGCGCGCGCTCGGAC 3156
Qy 1051 PheSerSerProAsnProLeuCysLeuGlyLeuCysProCysArgGlnGluHisIleGly 1070
Db 3157 ACCTCAGCTCGCGGCCCTACTCTCTGCT-GCCTGTGTGTGC-----CTGGGG 3203
Qy 1071 MetProMetAsnThrPro 1076
Db 3204 GCTACTGCCCCCAACTCCT 3221
RESULT 5
US-10-257-174-11
; Sequence 11, Application US/10257174
; Publication No. US20040034194A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.

Db 1912 GGCACGAGAAATACATCTTCTGGGAAACACGCTCTGTGGAAGAGCGCTGCATGACTTG 1971
Qy 611 LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630
Db 1972 CTTTACCCACAGACCTGGCCCTTGGCCGGTGTACTGGATCTTACTGTCATCACAGATATTGACCCA 2031
Qy 631 AspHisArgIysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgIysAspPro 650
Db 2032 GACACCGGAAGCTCAGCCAGCTTAGAGGCCATGATCCGCTTCTCACCAGAAAGGACCCA 2091
Qy 651 AspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValAlaThrAla 670
Db 2092 GACCTGGAGTGTGACGAGGAGCTGCTCCGGAGGTGCTGTTTCACGCGGTGTGACAGCC 2151
Qy 671 ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisVal 690
Db 2152 CCCATGGAAAGCTTACTGGACAGCGCTGGCCCTCAACATGTCTCCAGGAGTCTGAACACGTG 2211
Qy 691 ValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGly 710
Db 2212 GTGGACATGGCCCTTCTGGGCACCCGGGCTGGCTCTCTGAAAGCAGCTTGTTCGTGGGC 2271
Qy 711 SerGluLysValSerAspArgIysPheLeuThrProGluAspGluAlaSerValPheThr 730
Db 2272 TCCGAGAAAGTCTCCGACAGGAAGTTCTTGACACCTGAGGACGAGCGAGGTGTTTCAAC 2331
Qy 731 LeuAspArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheVal 750
Db 2332 CTGGACCGCTTCCCGCTGTGTGTACCCGCCAGCGCTCAGAGCATCTCTGTCGAGCTTCGTC 2391
Qy 751 PheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyLeuProMetValValThrAla 770
Db 2392 TTCAACTCCGCTGGGAGAGGACAGAAAGTGCGGGTGAACCCATGTGTGGTGGACGGCA 2451
Qy 771 SerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaGlyVal 790
Db 2452 AGCACAGCTGTGGCGGTGACCGTGGACAGAGGACAGCCATTCTGCAGCGCGGCGTC 2511
Qy 791 GlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThr 810
Db 2512 CAAATGAAGCTGGAATTCCTCCAGCGCAAAATTCCTGGCGCGCAACGGCGGAGTGCAGCACT 2571
Qy 811 ValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAsp 830
Db 2572 GTGGATGGCGCGTGACACAGAGCTCGGAGGACAGTGAICTGAGACTGCTTCGTATCGAC 2631
Qy 831 AsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGlu 850
Db 2632 AACACGGGTTTATTCTGATCTCCAAGAGGTCCCGAGAGACGGGAAGATTTCTGGGGGAG 2691
Qy 851 ValAspGlyValAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMet 870
Db 2692 GTGGATGGTGTCTCTGACCCAGCTGCTCAGATGGGGGTGTTACGCCAAGTACTATG 2751
Qy 871 TyrAspTyrGlnAlaMetCysLysProSerSerHisHisSerAlaAlaGlnProLeu 890
Db 2752 TATGACTATCAGGCCATGTGCAAAACCTCGAGTCAACACACAGTCAGCCAGCCGCCCTG 2811
Qy 891 ValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnLeuValLeu 910
Db 2812 GTCAGGCCAAATTTCTGCTTCTTTCAGCGGACCCAGGTGGCTGTGTCAGGAGTGGTGTG 2871
Qy 911 PheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSer 930
Db 2872 TTCCTCTGGAGTGGAGTGTCTGGGCTCTCTGTGTACGACAGAGGGGCCGAGGCC----- 2925
Qy 931 ValPheHisSerHisLysHisLysGlnAspProLeuGlnProCysAspThrGlu 950
Db 2926 -----CACAAACACAGAGAGCAGGACCCGCTGCAGCGCTGCAGACGGAG 2970
Qy 951 TyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGly 970

Db 2971 TACCCTGCTGTCTGTGTACACGCGGCCATCCGGAGGCCAACGGGATCTGTGGAGTGGGG 3030
Qy 971 ProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuVal 990
Db 3031 CCTGTGCAGAGGTATTTGTGTGTGCAGCAGATTCCCAACAGTAACCTCTCTCTCTGGTG 3090
Qy 991 ThrAspProThr--CysAspCysSerIlePheProValLeuGlnGluAlaThrGlu 1009
Db 3091 ACAGACCCCACTTCTGCAGATGGCTCGGTCTGAGATATTGACCTTAACAGTGGCT 3150
Qy 1010 ValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArg 1029
Db 3151 TCTGCACATAATGCTCTCTCAATGTGACCGATGCGCTCCCGAAGCTCCGCGCGCA 3210
Qy 1030 ProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspArgGlyTrpAla 1049
Db 3211 CCAGACTCTCTGCAGCGCTTCCATCCAGAGGAGAATGCCAGGACTGCGCGCGCTCG 3270
Qy 1050 GlyPheSerSerProAsnProLeuCysLeuGlyLeuCysProCysArgGlnGluHisIle 1069
Db 3271 GACACTCAGCTCGCGGCCCTTACTCTGCT-GCCTGTGTGTGC-----CTG 3317
Qy 1070 GlyMetProMetAsnThrPro 1076
Db 3318 GGGGCTACTGCCCAACTCT 3338
RESULT 6
US-10-257-022-27
; Sequence 27, Application US/10257022
; Publication NO. US20030211499A1
; GENERAL INFORMATION:
; APPLICANT: REDDY, Roopa
; APPLICANT: THORNTON, Michael
; APPLICANT: BOROWSKY, Mark L.
; APPLICANT: TANG, Y. Tom
; APPLICANT: KHAN, Farrah A.
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: YAO, Monique G.
; APPLICANT: SANJANWALA, Madhusudan M.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: NGUYEN, Dannie B.
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: YUE, Henry
; APPLICANT: SEILHAMER, Jeffrey J.
; APPLICANT: WALIA, Narinder K.
; APPLICANT: LAL, Preeti
; APPLICANT: KEARNEY, Liam
; APPLICANT: WALSH, Roderick T.
; APPLICANT: LU, Dyrung Aina M.
; APPLICANT: LU, Yan
; APPLICANT: GREENE, Barrie D.
; APPLICANT: RAUMANN, Brigitte E.
; APPLICANT: Arvizu, Chandra S.
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PI-0067 USN
; CURRENT APPLICATION NUMBER: US/10/257,022
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: US01/11206
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/195,595
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/196,872
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/199,020
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/200,552
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/202,348
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/203,495
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 30

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; SOFTWARE: PERL Program
; SEQ ID NO 27
; LENGTH: 4125
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7473443CB1
US-10-257-022-27

Alignment Scores:
Pred. No.: 0 Length: 4125
Score: 3808.00 Matches: 750
Percent Similarity: 80.90% Conservative: 4
Best Local Similarity: 80.47% Mismatches: 14
Query Match: 66.50% Indels: 164
DB: 18 Gaps: 2

US-09-833-222A-10 (1-1090) x US-10-257-022-27 (1-4125)
Qy 11 AspArgValLysLeuTrpAlaAspThrPheGlyAspLeuTyrAsnThrValThrLys 30
Db ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1120 GAAACAGTGAAGCTATGGCTGACACCTTCGGCGGGGACCTGTATAACACTGTGACCAA 1179
Qy 31 TyrSerGlySerLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysile 50
Db ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1180 TACTCAGGCTCTCTCTTCTGCTGCAGAAGAAGTACAAAGATGTGGAGTCCAGTCTGAAGATC 1239
Qy 51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
Db ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1240 GAGGAGTGGATGGCTTGGAGCTGGTGAAGATTTCTCAGAGGACATGGAGAACTGCTG 1299
Qy 71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn 90
Db ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1300 CGGAGAAAGTCGAGGCGGTCCAGAACTGTGTGAAGCTGCCGAGAGGCCGACCTGAC 1359
Qy 91 HisGluPheAsnGluSerLeuVal-
Db ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
1360 CACGAATCAATGAATCCCTGGTGGAACTCGCGTGGGAGTTGGCGTGGGATGTCCGTG 1419
Qy 98 ----- 98
Db 1420 ACGCAGTCCGCGTGGGAGTTGGCGTGGGATGTCCGTGACGACGTCCGCGTGGGAGTT 1479
Qy 98 ----- 98
Db 1480 GCGTGGGGATGTCCATAACGCTGTCGCGGCTGGGAGTTGGCGTGGGATGTCCGTGAGG 1539
Qy 98 ----- 98
Db 1540 CAGTCCGCGTGGGAGTTGGCGTGGGATGTCCGTGACGACGTCCGCGTGGGAGTTGGC 1599
Qy 98 ----- 98
Db 1600 GTGGGAGTCCGTGACGACATCCGCGTGGGAGTTGGCGTGGGATGTCCGTGAGGACAG 1659
Qy 98 ----- 98
Db 1660 TCCGCGTGGGAGTTGGCGTGGGATGTCCGTGACGACGTCCGTGGGAGTTTCAGTGCC 1719
Qy 98 ----- 98
Db 1720 CAGCGCGCGCGGGGTGCTTGTGTAGACTCTGATGGCGCGCGCGCGCGCGCTCTCG 1779
Qy 98 ----- 98
Db 1780 TCCTCTCACCTGCGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1839
Qy 99 ----- PheAspTyrTyrAsnSerValLeuIleAsnGlu 109
Db 1840 TCCGTGGGCTCACCCGCTCCACCCAGTTCGACTATTACAACTCGGTCTCTGATCAACGAG 1899
Qy 110 ArgAspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAla 129
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Db 1900 AGGACGAGAAAGGCAACTTCGTGGAGCTCGGGCCGAGTTCCTCTCTGGAGTCCAATGCT 1959
Qy 130 HisPheSerAsnLeuProValAanThrSerIleSerSerValGlnLeuProThrAsnVal 149
Db 1960 CACTTCAGCAACCTGCCGCTGAACACCTCCATCAGCAGCGTGCAGCTGCCCAACAGTG 2019
Qy 150 TyrAsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaVal 169
Db 2020 TACAACAAGACCCAGATATTTAAATGGAGTCTACATGTCTGAAGCTTTGAATGCTGTC 2079
Qy 170 PheValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThr 189
Db 2080 TTCGTGGAGAACTTCCAGAGAGACCCAACTGTGACCTGGCAATATTTTGGCAGTGCAACT 2139
Qy 190 GlyPhePheArgIleTyrProGlyIleLysTyrThrProAspGluAsnGlyValIleThr 209
Db 2140 GGATCTTCCAGGATCTATCCAGGTATAAATGGACACCTGATGAGATGGAGTCACTACT 2199
Qy 210 PheAspCysArgAsnArgGlyTyrTyrIleGlnAlaAlaThrSerProLysAspIleVal 229
Db 2200 TTTGACTGCCGAAACCGCGCTGTGTACATTCAGCTGTACTTCTCCCAAGGACATAGTG 2259
Qy 230 IleLeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThr 249
Db 2260 ATTTTGGTGGACGTGAGCGCGATGTAAGGGGCTGAGGATGACTATTGCCAAGCACACC 2319
Qy 250 IleThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAanIleIleAlaTyrAsn 269
Db 2320 ATCACCAACCATTTGGNACCCCTGGGGAGAGTACTTTCATTATATCATAGCGTACAT 2379
Qy 270 AspTyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAsp 289
Db 2380 GACTAGCTCCATTACATCGAGCTTGTGTTAAAGGATCCTCGTCAGAGCGGACCGAGAC 2439
Qy 290 AsnArgGluHisPheLysLeuValGluLeuMetValLysGlyValGlyValVal 309
Db 2440 AATTCGAGAGCATTTTCAAACTGCTGGTGGAGAGTTGATGTCAAAGGTGTGGGGTGGT 2499
Qy 310 AspGlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGly 329
Db 2500 GACCAAGCCCTGAGAGAGCTTCCAGATCTCAGACAGTTCACAGAGGCCAAGCAAGGA 2559
Qy 330 SerLeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluPro 349
Db 2560 AGCCTCTGCAACCCAGGCCATCATGCTCATCAGCGCGCGCTGGAGGACTACGAGCCG 2619
Qy 350 ValPheGluLysTyrAsnTyrProAspCysLysValArgValPheThrTyrLeuIleGly 369
Db 2620 GTGTTTGGAGAGTATTAACCTGGCCAGACTGTAAAGTCCGAGTTTTCCTTACCTCATTTGGG 2679
Qy 370 ArgGluValSerPheAlaAspArgMetLysTyrIleAlaCysAsnAsnLysGlyTyrTyr 389
Db 2680 AGAAGAGTGTCTTTGCTGACCCATGAGTGGATTGCATGCACAACAAGGCTACTAC 2739
Qy 390 ThrGlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeu 409
Db 2740 ACGCAGATCTCAACGCTGGCGGACACCCAGGAGAACGTGATGGAATACCTCGACGCTGCTC 2799
Qy 410 SerArgProMetValIleAsnHisAspHisAspIleThrThrGluAlaTyrMetAsp 429
Db 2800 AGCGCGCCCATGTGTATCAACCCAGCACCATCATCTCTGGACAGAGGCTTACATGGAC 2859
Qy 430 SerLysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetPro 449
Db 2860 AGCAAGCTCTCAGCTCGCAGGCTCAGAGCTGACACTGCTCACCCTGTGGCCATGCCA 2919
Qy 450 ValPheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySer 469
Db 2920 GTCTTCAGCAAGAAGAACCAACCGCATCCCATGGCATTTCTCTGGGTGTGGTGGGTCA 2979
Qy 470 AspValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGly 489
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Db 2980 GATGGCCCTGAGAGAGCTGATGAAGCTGGCGCCCGGTACAAGCTTGGAGTGACCGGA 3039
Qy TyrAlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeu 509
Db 3040 TACGCCCTTCTGAACACCAACAATGGGTATCATCTCTCCATCCCGACCTCCGCGCCCTG 3099
Qy TyrArgGluGlyLysLeuLysProLysProLysProAsnTyrAsnSerValAspLeuSerGlu 529
Db 3100 TACAGAGAGGGGAAGAAATAAACCACCAACCTTAACATACAAAGTGTGGATCTCTCCGAA 3159
Qy ValGluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGly 549
Db 3160 GTGGAGTGGGAAGACCAAGGCTGATCTCTGAGAACGCCATGATCAATAGGAAACAGGT 3219
Qy ThrLeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThr 569
Db 3220 ACTCTCTCGATGGATGTGAAGTTCCGATGGATAAAGGAAGCGAGTTCTTTTCCGTACC 3279
Qy AsnAspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSer 589
Db 3280 AATGACTACTTCTTCACGGACATCAGCACACCCCTTTTCAGTTTGGGGTGGTGCTGTC 3339
Qy ArgGlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAsp 609
Db 3340 CGGGGCCACGAGAATAATATCTTCTGGGGAACACGCTCTGTGGAAGAAAGCGCTGCATGAC 3399
Qy LeuLeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAsp 629
Db 3400 TTGCTTTCACCCAGACTTGGCGCCCTGGCGGGTACTGGATCTACTGCATCACAGATATTGAC 3459
Qy ProAspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAsp 649
Db 3460 CCAGACCACCGGAAGCTACCCAGCTAGAGCCATGATCCGCTTCTCCACGAGGAGAC 3519
Qy ProAspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValThr 669
Db 3520 CCAGACCTGGAGTGTGACGAGGAGCTGGTCCGGGAGTGCTGTTGACCGGGTGGTGACA 3579
Qy AlaProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHis 689
Db 3580 GCCCCCATGGAAGCCTACTGGACAGCGCTGGCCCTCAACATGTCCGAGGAGTCTGAACAC 3639
Qy ValValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheVal 709
Db 3640 GTGGTGGACATGCGCTTCTGGGCACCCGGGCTGGCTCTCTGAGAAGCAGCTTGTTCGTG 3699
Qy GlySerGluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPhe 729
Db 3700 GGCTCCGAGAAGGTCTCCGACAGGAAGTTCTCTGACACCTGAGGACGAGGCGAGCGTGTTC 3759
Qy ThrLeuAspArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPhe 749
Db 3760 ACCCTGGACCGCTTCCGCTGTGGTACCAGCGCCTCAGAGCATCTCTGTGGACGCTTC 3819
Qy ValPheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThr 769
Db 3820 GTCTTCAACCTCGCTGGGCGAGAAGACCA-----GGACGCCCTTCTGCCAAAGGC 3870
Qy AlaSerThrAlaValAlaValThrValAspLysArg 781
Db 3871 CTTCCACCACCACTTTTGCCAAACCATCTCTCAAGCGT 3906
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RESULT 7

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US-10-924-081-5
; Sequence 5, Application US/10924081
; Publication No. US20050095678A1
; GENERAL INFORMATION:
; APPLICANT: PARKER, David
; APPLICANT: XU, Xianghong
; APPLICANT: KHAWAJA, Afshen
; APPLICANT: SNUCH, Terrance P.
; TITLE OF INVENTION: NOVEL RAT CALCIUM CHANNEL SUBUNITS AND
; RELATED PROBES, CELL LINES AND METHODS
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; FILE REFERENCE: 381092001400
; CURRENT APPLICATION NUMBER: US/10/924,081
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: PCT/CA2004/001550
; PRIOR FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US 60/497,096
; PRIOR FILING DATE: 2003-08-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3598
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-924-081-5

Alignment Scores:
Pred. No.: 0 Length: 3598
Score: 3422.50 Matches: 626
Percent Similarity: 77.54% Conservative: 192
Best Local Similarity: 59.34% Mismatches: 220
Query Match: 59.77% Indels: 18
DB: 22 Gaps: 6
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US-09-833-222A-10 (1-1090) x US-10-924-081-5 (1-3598)

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Qy 13 ValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLysTyrSer 32
Db 124 GTGAAGCTCTGGCCCTCCGCTTTTGGTGGGAGATAAAATCCATTCTGCTGCCAAGTACTCG 183
Qy 33 GlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIleGluGlu 52
Db 184 GGTTCACACCTTCTGCAAAAGAAATACAAAGAGTATGAGAAAGACGCTTGCCATTGAAGAA 243
Qy 53 ValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArg 72
Db 244 ATCGACGGTCTCCAACTGGTGAAAAAGCTGGGCCAAGAACATGGAAGAGATGTTTCAAG 303
Qy 73 LysValGluAlaValGlnAsnLeuValGluAlaGluGluAlaAspLeuAsnHisGlu 92
Db 304 AAGTCGAGGAGTGGCGGCTCTCGTGGAGGCTGACGAGAGACACCTGAAGCATGAA 363
Qy 93 PheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArgAspGlu 112
Db 364 TTTGACGCGCAGCTTGCAGTATGAATACTTCAATGCCGTCTGATCAACGAGAGACAAA 423
Qy 113 LysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPheSer 132
Db 424 GATGGGAACCTTTTGGAAATTGGGAAGGAGTTTCATCTTGGCCCCCAATGACCATTTAAT 483
Qy 133 AsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyrAsnLys 152
Db 484 AATTTGCCCTGTGAACATCAGTCTGAGTGATGTCCAAAGTCCCAACGACATGTACACAAA 543
Qy 153 AspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheValGlu 172
Db 544 GATCCTGCCATAGTCAATGGAGTGATTGGTCTGAATCTCTAAACAAAAGTTTTTGTAGAC 603
Qy 173 AsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePhe 192
Db 604 AACTTCGATCGGGACCCGCTCTCTCATATGCGAGTAGTCTTGGAAAGTGCAAGGGCTTTTC 663
Qy 193 ArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPheAspCys 212
Db 664 AGACAGTACCCAGGAGTTAAATGGGAACCAAGACAGAGATGGAGTCAATGCCCTTTGACTGC 723
Qy 213 ArgAsnArgGlyTrpTrpIleGlnAlaThrSerProLysAspIleValIleLeuVal 232
Db 724 AGGAACAGAGAAATGTTACATCCAGGCAGCAACTTCTCCAAAGGATGTGTGTCATTTGGTG 783
Qy 233 AspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThrThr 252
Db 784 GACGTGACGGGAGCATGAAAGGACTCCGCTTGACCATGCGCAAGCAACAGTCTCTCTCG 843
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Db 2971 TGTGAAGACTGCTCAAGTCTTTGTTCATCCAGCAAAATCCCAAGTAGCAATCTGTTTCATG 3030
 Qy 989 LeuValThrAspProThrCysAspCysSerIlePheProValLeuGlnGluAlaThr 1008
 Db 3031 GTGGTGGTGACAGTAGCTGTCTCTGTGAGTCTGTGGCTCTCTATCCACCATGGCACCCATT 3090
 Qy 1009 GluValLysTyrAenAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArg 1028
 Db 3091 GNAATCAGGTATATGAATCCCTTAAGTGTGAACGGTTAAAGGCTCAGAAGATCAGACGA 3150
 Qy 1029 ArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspArgGlyTyr 1048
 Db 3151 CGTCCGAATCCGCCACGGCTTCCATCTCTGAGGA-----GNAATGCCAGAGAGTGTGG 3203
 Qy 1049 AlaGlyPheSerProAenProLeuCysLeuGlyLeuCysPro 1063
 Db 3204 GGGTGCATCAAGTCTCCAGGCCCCAGGTGGCCTTGTGCTGCTGCC 3248

RESULT 8

US-09-728-628-12
 : Sequence 12, Application US/09728628
 : Patent No. US20020009786A1
 : GENERAL INFORMATION:
 : APPLICANT: Tang, Y. Tom
 : APPLICANT: Zhou, Ping
 : APPLICANT: Goodrich, Ryle
 : APPLICANT: Liu, Chenghua
 : APPLICANT: Asundi, Vinod
 : APPLICANT: Xue, Aidong J.
 : APPLICANT: Zhang, Jie
 : APPLICANT: Zhao, Qing A.
 : APPLICANT: Ren, Feiyan
 : APPLICANT: Drmanac, Radoje T.
 : TITLE OF INVENTION: No. US20020009786A1el Nucleic Acids and
 : FILE OF INVENTION: Polypeptides
 : FILE REFERENCE: 791CIP2C
 : CURRENT APPLICATION NUMBER: US/09/728, 628
 : PRIOR FILING DATE: 2000-12-01
 : PRIOR APPLICATION NUMBER: 09/552,929
 : PRIOR FILING DATE: 2000-04-18
 : NUMBER OF SEQ ID NOS: 14
 : SOFTWARE: pt_FL_genes Version 2.0
 : SEQ ID NO 12
 : LENGTH: 3528
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: (213)..(3206)
 US-09-728-628-12

Alignment Scores:
 Pred. No.: 0 Length: 3528
 Score: 3421.50 Matches: 629
 Percent Similarity: 77.83% Conservative: 189
 Best Local Similarity: 59.85% Mismatches: 212
 Query Match: 59.75% Indels: 22
 DB: 9 Gaps: 7

US-09-833-222a-10 (1-1090) x US-09-728-628-12 (1-3528)

Qy 12 ArgValLysLeuThrPheAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLysTyr 31
 Db 51 AGGGTGAAGCTCTGGGCTCGGCTTTTGGTGGGAGATAAAATCCATTGCTGCTAAGTAC 110
 Qy 32 SerGlySerLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIleGlu 51
 Db 111 TCCGGTTCACGCTTCTGCAAAAGAAATACAAAGAGTATCAGAAAGACGTTGCCATAGAA 170
 Qy 52 GluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArg 71
 Db 171 GAAATCGATGGCTCCAACTGGTAAAGAGAGCTGGCAAGAACATCGAAGAGATGTTTCAC 230

Qy 72 ArgLysValGluAlaValGlnAenLeuValGluAlaAalGluGluAlaAsePheLeuAenHis 91
 Db 231 AGAAATCTGAGCCCTCAGGCGCTCTGGTGGAGGCTGCAGAAAGACACACCTGGAACAT 290
 Qy 92 GluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAenGluArgAsp 111
 Db 291 GAATTTGATGCAGACTTACAGTATGAATACTTCAATGCTGTGCTGATAAATGAAGGAC 350
 Qy 112 GluLysGlyAenPheValGluLeuGlyAlaGluPheLeuLeuGluSerAenAlaHisPhe 131
 Db 351 AAAGCGGAAATTTTGGAGCTGGGAAAGGAATTCATCTTAGCCCCAAATGACCATTTT 410
 Qy 132 SerAsnLeuProValAenThrSerIleSerSerValGlnLeuProThrAenValTyrAsn 151
 Db 411 AATAATTTGCCCTGTGAACATCAGTCTAAGTGACGTCCTCAAGTACCAACGACATGTACAAC 470
 Qy 152 LysAspProAspIleLeuAenGlyValTyrMetSerGluAlaLeuAenAlaValPheVal 171
 Db 471 AAAGACCTTGCATTTGCAATGGGTTTATTTGGTCTGAATCTCTAAACAAGTTTGTGA 530
 Qy 172 GluAenPheGlnArgAspProThrLeuThrTyrGlnTyrPheGlySerAlaThrGlyPhe 191
 Db 531 GATACTTTTGACCGTGACCCATCTCTCATATGCGAGTACTTTTGGAAAGTGCAAAAGGGCTTT 590
 Qy 192 PheArgIleTyrProGlyIleLysTyrThrProAspGluAenGlyValIleThrPheAsp 211
 Db 591 TTTAGGCAGTATCCGGGATTAAATGGGAACAGATGAGATGGAGTCAATTCGCTTCGAC 650
 Qy 212 CysArgAsnArgGlyTyrTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeu 231
 Db 651 TGCAGGAACCGAAATGGTACATCCAGGCGAGCAACTTCTCCGAAAGACGTTGTCATTTA 710
 Qy 232 ValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThr 251
 Db 711 GTTGAGCTCAGTGGCAGCATGAAGAGCTCCGCTGCTGACTATCGGAAGCAAAAGCTCTCA 770
 Qy 252 ThrIleLeuAspThrLeuGlyGluAenAspPheValAsnIleIleAlaTyrAsnAspTyr 271
 Db 771 TCCATTTTGGATACACTTGGGGATGATGACTCTTCAACATAATTCCTTATATAGGAG 830
 Qy 272 ValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsnArg 291
 Db 831 CTTCACTATGTGGAACCTTGTCCCTGGAATGGAACCTTGTGGTCAAGCCGACAGGACAAACA 890
 Qy 292 GluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAspGln 311
 Db 891 GAGCACTTCAGGAGGAGCATCTGGACAACTTTTCGCCAAAGGAATGGAATGTTGGATATA 950
 Qy 312 AlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySerLeu 331
 Db 951 GCTCTGAATGAGGCTTCAACATTTCTGAGTGATTTTCAACCCACACGCGGACAAAGGATATC 1010
 Qy 332 CysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProValPhe 351
 Db 1011 TGCAGTCAAGCCCATCATGTCTATACTGATGGGCGGTGGACACCTATGATACAATCTTT 1070
 Qy 352 GluLysTyrAsnTyrProAspCysLysValArgValPheThrTyrLeuIleGlyArgGlu 371
 Db 1071 GCATAATCAATTGGCCAGATCAAAAGGTTCCATCTTCACATACCTCATTTGACCGAGAG 1130
 Qy 372 ValSerPheAlaAspArgMetLysTyrIleAlaCysAsnAsnLysGlyTyrTyrThrGln 391
 Db 1131 GCTGCGTTTGCAGACAACTAAAGTGGATGGCTGTGCCCAACAAGAGATTTTTTACCCAA 1190
 Qy 392 IleSerThrLeuAlaAspThrGlnGluAenValMetGluTyrLeuHisValLeuSerArg 411
 Db 1191 ATCTCCACCTTGGCTGATGTGAGGAGAAATGTCATGGAATACCTTCACCTGCTTACCGG 1250
 Qy 412 ProMetValIleAsnHisAspHisAspIleIleTyrThrGluAlaTyrMetAspSerLys 431
 Db 1251 CCCAAGTATCATGCCAGGAGCATGATGTGGTGTGGACCGAAGCTTACATTGACAGCACT 1310
 Qy 432 LeuLeuSerSerGlnAlaGlnSerLeuThr-----LeuLeuThrThr 445

Db 1311 CTC-----CCTCAGGCACAAAAGCTGACTGATGATCAGGCGCCCGCTCTGATGACCACCT 1364
Qy 446 ValAlaMetProValPheSerLysLysAenGluThrArgSerHisGlyIleLeuLeuGly 465
Db 1365 GTAGCCATGCTGCTGTTAGTAGCAGACAGACCAACAGATCGAAGGCGCATCTCTGGGA 1424
Qy 466 ValValGlySerAspValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeu 485
Db 1425 GTGGTTGGCAGATGCTCCAGTGAAGAACTTCTGAAGACCATCCCCCAATAACAAGTTA 1484
Qy 486 GlyValHisGlyTyrAlaPheLeuAenThrAsnAsnGlyTyrIleLeuSerHisProAsp 505
Db 1485 GGGATTCCAGGTTATGCTTTGCAATCACAATAAATGGATATATCTCTGACGCGATCCGGAA 1544
Qy 506 LeuArgProLeuTyrArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerVal 525
Db 1545 CTGAGCTGCTGTACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1601
Qy 526 AspLeuSerGluValGluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsn 545
Db 1602 GACCTCTCTGAGTGGAGTGGGAGACCGAGATGACGTGTGAGAAATGCTATAGTGAAT 1661
Qy 546 ArgGluThrGlyThrLeuSerMetAspValLysValProMetAspLysGlyLysArgVal 565
Db 1662 CGAAGACGCGGGAAGTTTTCATCGAGGTGAAGAGACAGTGGACAAAGGGAACCGGTT 1721
Qy 566 LeuPheLeuThrAenAspTyrPhePheThrAspLysSerAspThrProPheSerLeuGly 585
Db 1722 TTGGTGTGACAAATGACTACTATTATACAGACATCAAGGGTACTCTCTTCAGTTTAGGT 1781
Qy 586 AlaValLeuSerArgGlyHisGlyGlyTyrIleLeuLeuGlyAsnThrSerValGluGlu 605
Db 1782 GTGGCGCTTTCCAGAGTCTATGGGAAATATTTCTCCGAGGGAATGTAAACCATCGAAGAA 1841
Qy 606 GlyLeuHisAspLeuLeuHisProAspLeuAlaGlyAspTrpIleTyrCysIle 625
Db 1842 GGCCTGTCATGACTTAGAACATCCGATGTCGTCTGTCAGTTAGACGATTAAGCTCTACCTA 1901
Qy 626 ThrAspIleAspProAspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeu 645
Db 1902 ACTGACCTCACCTCAGCAGCCGCATCTCTCTCAGTTAGACGATTAAGCTCTACCTA 1961
Qy 646 ThrArgLysAspProAspLeuGluCysAspGluLeuValArgGluValLeuPheAsp 665
Db 1962 AAAGGCAAGAACCTCTGCTCCAGTGTGATAAAGAAATGATCCAAGAGTCCCTTTTGAC 2021
Qy 666 AlaValValThrAlaProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGlu 685
Db 2022 GCGGTGGTGAAGTCCCGCCCATTTGAAGCGTATTGGACCAAGCCTGGCCCTCAACAAATCTGA 2081
Qy 686 GluSerGluHisValValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSer 705
Db 2082 AATTCTGACAGGCGTGGAGGTTGCTCTCTCGGACTCGACGGCGCTCTCCGAATC 2141
Qy 706 SerLeuPheValGlySerGluLysValSerAspArgLysPheLeuThrProGluAspGlu 725
Db 2142 AACCTGTTGTCGGGCTGAGCAGCTACCAATCAGGACTTCTCTGAAAGCTGGTGACAAG 2201
Qy 726 AlaSerValPheThrLeuAspArgPheProLeuTyrTrpArgGlnAlaSerGluHisPro 745
Db 2202 GAGAACATTTTAAACGCAGACCAATTTCCCTCTCTGTTACGAGAGCGCGTGAAGAGATT 2261
Qy 746 AlaGlySerPheValPheAenLeuArgTyrAlaGluGlyProGluSerAlaGlyGluPro 765
Db 2262 CCAGGAGCTTCTCTACTCGATCCCATTCGACCTGGACCA-----GTCAATAAAGC 2315
Qy 766 MetValValThrAlaSerThrAlaValAlaValThrValAspLysArgThrAlaIleAla 785
Db 2316 AATGTGTGACAGCAAGTATCATCCATCCAGCTCTCTGATGAACGGAATCTCTGTGGTG 2375
Qy 786 AlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPheThrAlaAlaThr 805

Db 2376 GCAGCTGTAGGCATTCAGATGAACCTGAATTTTCCAAAGGAAGTTCTGGACTGCCAGC 2435
Qy 806 ArgGlnCysSerThrValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAsp 825
Db 2436 AGACAGTGTCTCCCTGGATGGCAATGCTCCATCAGCTGTGATGATGAGACTGTGAAT 2495
Qy 826 CysPheValIleAspAenGlyPheIleLeuIleSerLysArgSerArgGluThrGly 845
Db 2496 TGTACTCATAGACAATAATGATTTATTTGGTGTCTGAAGACTACACAGACTGGA 2555
Qy 846 ArgPheLeuGlyValValAspGlyAlaValLeuThrGlnLeuSerMetGlyValPhe 865
Db 2556 GACTTTTTTGGTGAGATCGAGGAGCTGTGATGAACAAATTTGTAACATGGGCTCCTTT 2615
Qy 866 SerGlnValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisSer 885
Db 2616 AAAAGAAATACCTTTATGACTACCAAGCCATGTGTAGACCAACAAGGAAGCAGCGAT 2675
Qy 886 AlaAlaGlnProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeu 905
Db 2676 GCGCGCCCATGGCTCTGGATCCTTAATATGCTCTCTGACAGTAAATGATCATG 2735
Qy 906 GlnGluLeuValLeuPheLeuGluTyrSerValTrpGlySerTrpTyrAspArgGly 925
Db 2736 ACAGAACTTGTCTGTGTGGTGAATTTAACTCTGC-----AGTTGGTGGCATCCGAT 2792
Qy 926 AlaGluAlaLysSerValPheHisHisSerHisLysLysGlnAspProLeuGln 945
Db 2793 ATGACAGCTAAAGCC-----CAGAAATTTGAACAGACCTCGAG 2831
Qy 946 ProCysAspThrGluTyrProValPheValTyrGlnProAlaIleArgGluAlaAenGly 965
Db 2832 CCTTGTGATACTGAATATCAGCATTCGTCTCTGAGCGCACCATCAAGGAGACTACAGGG 2891
Qy 966 IleValGluCysGlyProCysGlnLysValPheValValGlnGlnIleProAsnSerAsn 985
Db 2892 AATATTGCTTGTGAAGACTGCTCAAGTCTTTGTATCAGCAATTTCCCAAGCAAC 2951
Qy 986 LeuLeuLeuLeuValThrAspProThrCysAspCysSerIlePheProValLeuGln 1005
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Qy 1006 GluAlaThrGluValLysTyrAenAlaSerValLysCysAspArgMetArgSerGlnLys 1025
Db 3012 GCACCATTTGAATCAGGTATAATGAATCCCTTAAGTGTCAACGCTTAAAGGCCAGAG 3071
Qy 1026 LeuArgArgArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAsp 1045
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Db 3126 GAGTG-TGGGGTGGCGCCGAGTCTCCAAAGCCCA 3157

RESULT 9

US-10-972-024-117
; Sequence 117, Application US/10972024
; Publication No. US20050221342A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 79IC14
; CURRENT APPLICATION NUMBER: US/10/972,024
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: PCT/US01/08655
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/668,317
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/695,783

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/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: 09/728, 628
/ PRIOR FILING DATE: 2000-12-01
/ PRIOR APPLICATION NUMBER: 09/783, 066
/ PRIOR FILING DATE: 2001-02-13
/ PRIOR APPLICATION NUMBER: 09/816, 828
/ PRIOR FILING DATE: 2001-03-22
/ NUMBER OF SEQ ID NOS: 584
/ SOFTWARE: Custom
/ SEQ ID NO 117
/ LENGTH: 3528
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (213)..(3203)
US-10-972-024-117

Alignment Scores:
Pred. No.: 0 Length: 3528
Score: 3421.50 Matches: 629
Percent Similarity: 77.83% Conservatives: 189
Best local Similarity: 59.85% Mismatches: 212
Query Match: 59.75% Indels: 22
DB: 24 Gaps: 7

US-09-833-222A-10 (1-1090) x US-10-972-024-117 (1-3528)

QY 12 ArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLysTyr 31
Db 51 AGGGTGAAGCTCTGGGCTCGGCTTTTGGTGGGAGATAAAATCCATTCGTGCTAAGTAC 110
QY 32 SerGlySerLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysLysGlu 51
Db 111 TCCGGTTCACAGCTCTCGCAAAAGAAATACAAAGAGATGAGAAAGACGTGCGCATAGAA 170
QY 52 GluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArg 71
Db 171 GAAATCGATGGCTCCAACTGGTAAAGAGCTGGCAAGAACATGGAAGAGATGTTTAC 230
QY 72 ArgLysValGluAlaValGlnAsnLeuValGluAlaGluAlaAspLeuAsnHis 91
Db 231 AAGAAGCTCTGAGCGCTCAGGCTGTGGTGGAGGCTGCAGAGAGACACCTCTGAAACAT 290
QY 92 GluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuLeuLeuAsnGluArgAsp 111
Db 291 GAATTTGATCGACACTTACAGTATGAATACTTCATGCTGTGCTGATTAATGAAGGAC 350
QY 112 GluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPhe 131
Db 351 AAAGACGGGAATTTTGGAGCTGGGAAGGAATTCATCTTAGCCCCAAATGACCAATTTT 410
QY 132 SerAsnLeuProValAsnThrSerLysSerValGlnLeuProThrAsnValTyrAsn 151
Db 411 AATAATTTGGCTGTGAACATCATCTAAGTGACGTCCAAAGTACCAACGAACATGTACAAC 470
QY 152 LysAspProAspLysLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheVal 171
Db 471 AAGACCTTGCATATGCTCAATGGGGTTTATGGTCTGAATCTTAAACAAAGTTTTTGTGA 530
QY 172 GluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhe 191
Db 531 GATAACTTTTGACGCTGACCATCTCTCATATGGCAGTACTTTTGGAAAGTGCAAGGGCTTT 590
QY 192 PheArgLysLeuProGlyLysTrpThrProAspGluAsnGlyValLysLeuThrPheAsp 211
Db 591 TTTAGGCAGTATCCGGGGATTAATGGGAACCCAGATGAGAATGGAGTATTCGCTTCGAC 650
QY 212 CysArgAsnArgGlyTrpTyrLysGlnAlaAlaThrSerProLysAspLysValLysLeu 231
Db 651 TGCAGAACCGAAATGGTATCATCCAGGACGCACTTCTCCGAAAGCGTGTGTCATTTTA 710
QY 232 ValAspValSerGlySerMetLysGlyLeuArgMetThrLysAlaLysHisThrLeuThr 251
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Db 711 GTTGAGCTCAGTGGCAGCATGAAAGGACTCCGCTGCACTATCGGAAGCAACAGTCTCA 770
QY 252 ThrLysLeuAspThrLeuGlyGluAsnAspPheValAsnLysLysLysLysLysLysLys 271
Db 771 TCCATTTTGGATACACTTGGGATGATGACTTCTTCAACATAATGCTTTATATATGAGAG 830
QY 272 ValHisTyrLysLeuProCysPheLysGlyLysLeuValGlnAlaAspArgAspAsnArg 291
Db 831 CTTCACATATGTGAACCTTGCCTGAATGGAACCTTTGGTCAAGCCAGCAGGACAAACAA 890
QY 292 GluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAspGln 311
Db 891 GAGCAGCTTCAGGAGCATCTGGACAACTTTTCGCCAAAGGAATTCGAATTTGGATATA 950
QY 312 AlaLeuArgGluAlaPheGlnLysLysGlnPheGlnGlnLysGlnLysGlnLysLeu 331
Db 951 GCTCTGAATGAGGCTTCAACATTCAGTGTATTTTCAACACACACGCGGACAAAGGATTC 1010
QY 332 CysAsnGlnAlaLysMetLeuLysSerAspGlyAlaValGluAspTyrGluProValPhe 351
Db 1011 TGCAGTCAAGCCATCATGCTCATTAAGTGGGCGGTGGACACCTATGATACAAATCTTT 1070
QY 352 GluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuLysGlyArgGlu 371
Db 1071 GCAAAATACAAATTTGGCCAGATCGAAAGGTTTCGATCTTCACATCTCATTGGACGAG 1130
QY 372 ValSerPheAlaAspArgMetLysTrpLysAlaCysAsnAsnLysGlyTyrTyrThrGln 391
Db 1131 GCTGGTGTTCAGACAACTTAAAGTGGATGGGCTGTGCCAACAAAGGATTTTTTACCCA 1190
QY 392 IleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSerArg 411
Db 1191 ATCTCCACCTTGGCTGATGTGCAGGAGATGTCATGGAATACCTTCACCTGCTTACCGG 1250
QY 412 ProMetValLysAsnHisAspLysLysLysLysLysLysLysLysLysLysLysLys 431
Db 1251 CCCAAAGTCTATCGACGAGCATGATGGTGGTGGACCGAGCTTACATTGCACGACT 1310
QY 432 LeuLeuSerSerGlnAlaGlnSerLeuThr-----LeuLeuThrThr 445
Db 1311 CTC-----CTTCAGCGCACAAAGCTGATGATGATCAGGCGCCGCTCTGATGACCAT 1364
QY 446 ValAlaMetProValPheSerLysLysAsnGluThrArgSerHisGlyLysLeuLeuGly 465
Db 1365 GTAGCATGCTGTGTGTAGTAAAGCAGACGAAACGAGATCGAAGGCGATTTCTTCTGGGA 1424
QY 466 ValValGlySerAspValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeu 485
Db 1425 GTGGTGGCACAGATGTCCAGTGAAAGAACTTCTGAAGACCATCCCAAAATACAAAGTTA 1484
QY 486 GlyValHisGlyTyrAlaPheLeuAsnThrAsnAsnGlyTyrLysLeuSerHisProAsp 505
Db 1485 GGGATTCAGGTTATGCTTTCGAATTCACAAATAATGGATATATCTCAGCATCCGAA 1544
QY 506 LeuArgProLeuTyrArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerVal 525
Db 1545 CTCAGGCTGCTGTACGAGAGGAAAAAAG---CGAAGGAAACCTTAACCTATAGTAGCGTT 1601
QY 526 AspLeuSerGluValGluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetLysLeu 545
Db 1602 GACCTCTCTGAGTGGAGTGGGAAGACCGAGATGACGTGTTGAGAAATGCTATGTTGAAT 1661
QY 546 ArgGluThrGlyThrLeuSerMetAspValLysValProMetAspLysGlyLysArgVal 565
Db 1662 CGAAAGCGGGGAAGTTTTCCATGGAGGTGAAGAGACAGATGGACAAAGGAAACCGGTT 1721
QY 566 LeuPheLeuThrAsnAspTyrPheThrAspLysSerAspThrProPheSerLeuGly 585
Db 1722 TTGGTGATGACAAATGACTACTATTATACAGACATCAAGGGTACTCTCTTTCAGTTAGGT 1781
QY 586 AlaValLeuSerArgGlyHisGlyGluTyrLysLeuLeuGlyAsnThrSerValGluGlu 605
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Db 1782 GTGGCGCTTTCCAGAGCTCATGGGAATATTTCTTCGAGGGGAATGTAAACCATCGAAGAA 1841
Qy 606 GlyLeuHisAspLeuLeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIle 625
Db 1842 GGCTTCATGACTTTAGAACATCCGATGTGCTTCCTGGCAGATGAATGCTCTACTGCAAC 1901
Qy 626 ThrAspIleAspProAspHisLeuArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeu 645
Db 1902 ACTGACCTACACCTGAGCACCAGCATCTGCTCAGTTAGAGCGATTAAAGCTCTACCTA 1961
Qy 646 ThrArgLysAspProAspLeuGluCysAspGluLeuValArgGluValLeuPheAsp 665
Db 1962 AAGGCCAAGAACCTCTGCTCCAGGTGTGAAGAAATGTGATCAAGAAAGTCCCTTTTGAC 2021
Qy 666 AlaValValThrAlaProMetGluAlaTyrTrpThrAlaLeuAlaLeuAenMetSerGlu 685
Db 2022 GCGGTGTGTAGTGCCCTCCCATTTGAAGCGTATTGGACACAGCTGGCCCTCAACAAATCTGAA 2081
Qy 686 GluSerGluHisValValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSer 705
Db 2082 AATTCTGACAAAGGCGTGGAGTTGCTCTCGGCACCTCGCACGGGCTCTCCAGAAATC 2141
Qy 706 SerLeuPheValGlySerGluLysValSerAspArgLysPheLeuThrProGluAspGlu 725
Db 2142 AACCTGTTTGTGGGGCTGAGCAGCTCACCAAATCAGGACTTCCTGAAAGCTGGTGGAAG 2201
Qy 726 AlaSerValPheThrLeuAspArgPheProLeuTrpTyrArgGlnAlaSerGluHisPro 745
Db 2202 GAGNACATTTTAACGCAGACCATTTCCCTCTGTTACCGAAGAGCGGTGAGCAGATT 2261
Qy 746 AlaGlySerPheValPheAenLeuArgTrpAlaGluGlyProGluSerAlaGlyGluPro 765
Db 2262 CCAGGGAGCTTCGTCTACTCGATCCCATTCAGCAGCTGGACCA-----GTCAATAAAGC 2315
Qy 766 MetValValThrAlaSerThrAlaValAlaValThrValAspLysArgThrAlaIleAla 785
Db 2316 AATGTGTGTGACAGCAAGTACATCCAGCTCTGGATGAACGGAATCTCTGTGGTG 2375
Qy 786 AlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThr 805
Db 2376 GCAGCTGTAGGCATTTCAGATGAACTTGAATTTTCCAAAGGAATTCGGACTGCCAGC 2435
Qy 806 ArgGlnCysSerThrValAspGlyProTyrTrpGlnSerCysGluAspSerAspLeuAsp 825
Db 2436 AGACAGTGTGTTCCCTCGATGGCAATTCCTCAGCTGTGTGATGATGAGACTGTGAAT 2495
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Db 2556 GACTTTTGTGTGATCGAGGAGCTGTGATGAACAAATTTGCTAACAAATGGGCTCCTTT 2615
Qy 866 SerGlnValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisSer 885
Db 2616 AAAAGAAATTACCTTTATGACTACCAAGCCATGTGTAGAGCCAAACAAGGAAGCAGCGAT 2675
Qy 886 AlaAlaGlnProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeu 905
Db 2676 GGCCGCCATGCCCTCTGGATCCTTATATAGCTTCTCTCTGCAATTAATGATCATG 2735
Qy 906 GlnGluLeuValLeuPheLeuGluTrpSerValTrpGlySerTrpTyrAspArgGly 925
Db 2736 ACAGAACTTGTCTTGTCTCTGGTGAATTTAACTCTGC---AGTTGGTGGCACTCCGAT 2792
Qy 926 AlaGluAlaLysSerValPheHisHisSerHisLysLysGlnAspProLeuGln 945
Db 2793 ATGACAGCTAAAGCC-----CAGAAATTTGAACACAGCCCTGGAG 2831
Qy 946 ProCysAspThrGluTyrProValPheValTyrGlnProAlaIleArgGluAlaAenGly 965
Db 2832 CCTTGTGATCTACTGAATATCCAGCAATTGCTCTCTGAGCGGCCCATCAAGGAGCTACAGGG 2891
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Qy 966 IleValGluCysGlyProCysGlnLysValPheValValGlnGlnIleProAenSerAen 985
Db 2892 AATATTGTTGTGAAGACTGCTCCAAGTCTTTGTTCATCCAGCAAAATCCCAAGCAGCAAC 2951
Qy 986 LeuLeuLeuLeuValThrAspProThrCysAspCysSerIlePheProProValLeuGln 1005
Db 2952 CTGTTTCATGTTGTGTGGACAGCAGCTGCTCTGTGAATCTGTGGCCCCCATCCCATG 3011
Qy 1006 GluAlaThrGluValLysTyrAenAlaSerValLysCysAspArgMetArgSerGlnLys 1025
Db 3012 GCACCATTCGAATCAGGTATATGAATCCCTTAAGTGTGAACGTCTAAAGGCCCAGAAG 3071
Qy 1026 LeuArgArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAsp 1045
Db 3072 ATCAGAAGGCCGCCAGAAATCTTGTTCATGGCTTCATCTCTGAG-----GAGAATGCAAGG 3125
Qy 1046 ArgGlyTrpAlaGlyPheSerSerProAenPro 1056
Db 3126 GAGTG-TGGGGGTGCGCCGAGTCTCCNAGCCCA 3157
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RESULT 10

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US-09-875-423-3
; Sequence 3, Application US/09875423
; Patent No. US20020081657A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: 21784, A NOVEL HUMAN CALCIUM CHANNEL
; FILE REFERENCE: 10448-059001
; CURRENT APPLICATION NUMBER: US/09/875,423
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3276
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-423-3
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Alignment Scores:
Pred. No.: 0 Length: 3276
Score: 3416.50 Matches: 628
Percent Similarity: 77.81% Conservative: 189
Best Local Similarity: 59.81% Mismatches: 212
Query Match: 59.67% Indels: 22
DB: 9 Gaps: 7
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US-09-833-222A-10 (1-1090) x US-09-875-423-3 (1-3276)

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Qy 33 GlySerLeuLeuGlnLysTyrLysAspValGluSerSerLeuLysIleGluGlu 52
Db 184 GGTTCGCCAGCTTCTGCAAAAGAAATACAAAGAGTATGAGAAAGACGTTGCCATAGAAGAA 243
Qy 53 ValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAenMetLeuArg 72
Db 244 ATTGATGGCTTCCAACTGGTAAAGAGCTGGCAAGAACATGGAAGAGATGTTTCACAG 303
Qy 73 LysValGluAlaValGlnAenLeuValGluAlaGluAlaAspLeuAenHisGlu 92
Db 304 AGTCTGAGGCCGCTCAGCGCTCTGGTGAGGCTGCACAAGAGCACACCTGAAACATGAA 363
Qy 93 PheAenGluSerLeuValPheAspTyrTyrAenSerValLeuIleAenGluArgAspGlu 112
Db 364 TTTGATCGACACTTACAGTATGAATCTTCAATGCTGCTGATATAAATGAAGGGGCAAA 423
Qy 113 LysGlyAenPheValGluLeuGlyAlaGluPheLeuLeuGluSerAenAlaHisPheSer 132
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Db 424 GACGGGAATTTTGGAGCTGGGAAGGAATTCATCTTAGCCCCCAATGACCAATTTTAAT 493
QY 133 AsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyrAsnLys 152
Db 484 AATTTGCTGTGAACATCAGCTAAAGTGAGCTCCAAAGTACCAACGAAACATGTGACAA 543
QY 153 AspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheValGlu 172
Db 544 GACCTGCAATTTGCAATGGGGTTTATGGTCTGAATCTCTAAACAAAGTTTTGTAGAT 603
QY 173 AsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePhe 192
Db 604 AACTTTGACCGTGACCCATCTCTCATATGCGCAGTACTTTTGGAAAGTGCAAAGGGCTTTTT 663
QY 193 ArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPheAspCys 212
Db 664 AGCAGTATCCGGGGATTAAATGGGAACCAAGATGAGAATGGAGTCAATTCGCTTCGACTGC 723
QY 213 ArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeuVal 232
Db 724 AGGACCGAAATTTGATATCCAGGCGAGCAACTTCTCCGAAAGACGTGGTCAATTTAGTT 783
QY 233 AspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThrThr 252
Db 784 GACGTCAGTGGCAGCATGAAGGACTCCGTCTGACTATCGCAAGCAACAGTCTCATCC 843
QY 253 IleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAspTyrVal 272
Db 844 ATTTTGGATACACTGGGGATGATGACTTCTTCAACATAATTCCTTATATAGGAGCTT 903
QY 273 HisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsnArgGlu 292
Db 904 CACTATGTGGAACCTTGCCGTGAATGGAACCTTTGGTGCAGGCCGACAGGCAACAAAGAG 963
QY 293 HisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValValAspGlnAla 312
Db 964 CACTTCAGGGAGCATCTGGACAAACTTTTCCCAAGGAATTTGGAATGTTGGATATAGCT 1023
QY 313 LeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnLysLeuCys 332
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QY 333 AsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProValPheGlu 352
Db 1084 AGTCAGGCCATCATGTCTAATCATGATGGGCGGTGGACACCTATGATACATCTTTGCA 1143
QY 353 LysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArgGluVal 372
Db 1144 AATACAAATTTGGCAGATCGAAAGGTTGCGCATCTTCACATACCTCATTTGGACGAGAGCT 1203
QY 373 SerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThrGlnIle 392
Db 1204 GCCTTTGACAGCAATCTAAAGTGGATGGGCTGTGCCAACAAAGGAATTTTTACCCAGATC 1263
QY 393 SerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSerArgPro 412
Db 1264 TCCACCTTGGCTGATGTGAGGAGATGTCATGGAATACCTTCACGTGTTAGCCGGCCCC 1323
QY 413 MetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSerLysLeu 432
Db 1324 AAAGTCATCGACCAGGAGCATGATGGTGTGGACCGAAGCTTACATTTGACAGCACTCTC 1383
QY 433 LeuSerSerGlnAlaGlnSerLeuThr-----LeuLeuThrVal 446
Db 1384 -----CCTCAGGCAAAAAGCTGACTGATGATCAGGGCCCCCTCTGATGACCACTGTA 1437
QY 447 AlaMetProValPheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyVal 466
Db 1438 GCCATCGCTGTGTTAGTAAGCAGACGAAACCCAGATCGAAGGGCATTCTTCTGGGAGTG 1497
QY 467 ValGlySerAspValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGly 486

Db 1498 GTTGGCACAGATGTCCCGAGTGAAAGAACTTCTGGAAGACCATCCCCAAATACAAAGTTAGGG 1557
QY 487 ValHisGlyTyrAlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeu 506
Db 1558 ATTTCAGGTTATGCGCTTTCACAAATAATGGATATATCTCTGACGATCCGGAACATC 1617
QY 507 ArgProLeuTyrArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAsp 526
Db 1618 AGGCTGCTGTACGAAGAAGAAAAAG---CGAAGGAAACCTTAACCTATAGTAGCGTTGAC 1674
QY 527 LeuSerGluValGluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArg 546
Db 1675 CTCTCTGAGTGGAGTGGGAAGACCAGATGACGTGTGTAGAAATGCTATGGTGAATCGA 1734
QY 547 GluThrGlyThrLeuSerMetAspValLysValProMetAspLysGlyLysArgValLeu 566
Db 1735 AAGACGGGGAAGTTTTTCATGGAGGTGAAGAAGACAGTGGACAAAGGGAACCGGTTTTG 1794
QY 567 PheLeuThrAsnAspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAla 586
Db 1795 GTGATGACAAATGACTACTATTATACAGACATCAAGGTACTCTCTTCAGTTTAGGTGTG 1854
QY 587 ValLeuSerArgGlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGly 606
Db 1855 GCGCTTTCAGAGGTTCATGGGAATATTTCTTCCGAGGGAATGTAACCATCGAAGAAGGC 1914
QY 607 LeuHisAspLeuLeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThr 626
Db 1915 CTGCAATGACTTAGAACATCCCGATGTCTTGGCAGATGAATGGTCTTACTGCAACACT 1974
QY 627 AspIleAspProAspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThr 646
Db 1975 GACCTACACCTTGAGCAGCCCATCTGTCTCAGTTAGAACGATTAAGCTCTACCTAAAA 2034
QY 647 ArgLysAspProAspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAla 666
Db 2035 GGCAAGAAGACCTCTGCTCCAGTGTGATAAAGAAATTCATCCAAGAGTCTCTTTTGACGC 2094
QY 667 ValValThrAlaProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGlu 686
Db 2095 GTGGTGAGTGCCCCCATTTGAAGCGTATTGGACAGCCTGGCCCTCAACAAATCTGAAAT 2154
QY 687 SerGluHisValValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSer 706
Db 2155 TCTGACAGGGCGTGAGGTTGCTCTCCGCACTCGCACGGCTCTCCAGAAATCAAC 2214
QY 707 LeuPheValGlySerGluLysValSerAspArgLysPheLeuThrProGluAspGluAla 726
Db 2215 CTGTTTGTGGGGCTGAGCAGCTCACCATCAGGACTTCTCTGAAAGCTCGCGACAGGAG 2274
QY 727 SerValPheThrLeuAspArgPheProLeuTyrTyrArgGlnAlaSerGluHisProAla 746
Db 2275 AACATTTTAAACGACAGACCATTTCCCTCTCTGTACCGAAGAGCCGCTGAGCAGATTCCA 2334
QY 747 GlySerPheValPheAsnLeuArgTrpLagLuglyProGluSerAlaGlyGluProMet 766
Db 2335 GGGAGCTTCGTCTACTCGATCCCATTCAGCACTGGACCA-----GTCAATAAAGCAAT 2388
QY 767 ValValThrAlaSerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAla 786
Db 2389 GTGGTGACAGCAAGTACATCCATCCAGCTCTCTGGATGAACCGGAAATCTCTCTGTGGGCA 2448
QY 787 AlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArg 806
Db 2449 GCTGTAGGCATTCAGATGAATTTGAACTTTTCCAAAGGAAGTTCTGGACTGCCACAGA 2508
QY 807 GlnCysSerThrValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCys 826
Db 2509 CAGTGTGCTTCCGTGGTGGCAAAATGCTCCATCAGCTGTGATGATGAGACTGTGAATTTGT 2568
QY 827 PheValIleAspAsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArg 846
Db 2569 TACCTCATAGACAAATAATGGATTTATTTGGTGTCTGAAGACTTACACACAGACTGGAGAC 2628

QY	173	AsnPheGlnArgAspProThrLeuThrTrpGlnTyrrPheGlySerAlaThrGlyPhePhe	192
Db	604	AACTTTGACCGTACCACATCTCATATGCGAGTACTTTTGGAAAGTGCAAAGGGCTTTTTT	663
QY	193	ArgIleTyrrProGlyIleIleTyrrThrProAspGluAsnGlyValIleThrPheAspCys	212
Db	664	AGCAGTATCCGGGGATTAAATGGGAACACAGATGAGAAATGGAGTCAATGCTTCGACTGC	723
QY	213	ArgAsnArgGlyTrpTyrrIleGlnAlaAlaThrSerProLysAspIleValIleLeuVal	232
Db	724	AGAAACCGAAATGGTATACATCCAGGCGCAACTTCTCCGAAAGACGTGGTCAATTTAGTT	783
QY	233	AspValSerGlySerMetLysGlyLeuAtqMetThrIleAlaLysHisThrIleThrThr	252
Db	784	GAGCTAGTGGCAGCATGAAGACTCCGTCGACTATCCGGAAGCAACAGTCTCATCC	843
QY	253	IleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrrAsnAspTyrrVal	272
Db	844	ATTTTGGATACACTTGGGGATGATGACTTCTTCAACATAATTCCTTATAATGAGGAGCTT	903
QY	273	HisTyrrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsnArgGlu	292
Db	904	CACATATGTGGAACTTTCCTCGAATGGAACCTTTTGGTCAAGCCGACAGCAAAACAAAGAG	963
QY	293	HisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAlaGlnAla	312
Db	964	CACCTTCAAGGAGCATCTGGCAACACTTTTCGCCAAGGAATTCGAATGTGGATATAGCT	1023
QY	313	LeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySerLeuCys	332
Db	1024	CTCAATGAGGCCCTTCAACATCTTGAGTGATTTCACACACAGCGGACAAAGGAATATCTGC	1083
QY	333	AsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrrGluProValPheGlu	352
Db	1084	AGTCAGGCCATCATGCTCAATACTGATGGCGGTGGACACCATATGATACAATCTTTGCA	1143
QY	353	LysTyrrAsnTrpProAspCysLysValArgValPheThrTyrrLeuIleGlyArgGluVal	372
Db	1144	AAATACAAATGGCCAGATCGAAAGGTTTGGCATCTTCACATACCTCATTTGGACGAGAGGCT	1203
QY	373	SerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrrTyrrGlnIle	392
Db	1204	CGCTTTGCAGACAATCTAAAGTGGATGGCTGTGCCCAACAAAGGATTTTTTACCCAGATC	1263
QY	393	SerThrLeuAlaAspThrGlnGluAsnValMetGluTyrrLeuHisValLeuSerArgPro	412
Db	1264	TCACACCTTGGCTGATGTGCAGGAGAAATGTCATGGAAATACCTTCACGTGCTTAGCCGGCCC	1323
QY	413	MetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrrMetAspSerLysLeu	432
Db	1324	AAAGTCATCGACCAGCAGCATGATGTGGTGGACCGAAGCTTACATTCACAGCACTCTC	1383
QY	433	LeuSerSerGlnAlaGlnSerLeuThr-----LeuLeuThrThrVal	446
Db	1384	-----CCTCAGGCACAAAAGCTGACTGATGATCAGGGCCCCGCTCCTGATGACCACTGTA	1437
QY	447	AlaMetProValPheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyVal	466
Db	1438	GCCATGCCCTGTGTTTGTAGTGAACGAGAACGAAACAGATCGAAGGGCAATCTTCTGGGAGTG	1497
QY	467	ValGlySerAspValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrrLysLeuGly	486
Db	1498	GTTCGCACAGATGTCCCGATGAAGAACTTCTGAGAACCATCCCCAAATACAAAGTTAGGG	1557
QY	487	ValHisGlyTyrrAlaPheLeuAsnThrAsnAsnGlyTyrrIleLeuSerHisProAspLeu	506
Db	1558	ATTACGGGTATGCCCTTGGCAATCAAAAATATGGATATATCTGACGCATCCGGAATCTC	1617
QY	507	ArgProLeuTyrrArgGluGlyLysLysLeuLysProLysProAsnTyrrAsnSerValAsp	526
Db	1618	AGGCTCTGTACGAAAGAGAAAAAG---CGAAGGAAACCTTAACATATATAGTACGCTTGAC	1674
QY	527	LeuSerGluValGluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArg	546
Db	1675	CTCTCTGAGGTGAGTGGGAAGACCGAGATGACGTGTTGAGAAATCTATGGTGAATCGA	1734
QY	547	GluThrGlyThrLeuSerMetAspValLysValProMetAspLysGlyLysArgValLeu	566
Db	1735	AAGACGGGGAAGTTTTTCCATGAGGTGAAGAAGACAGTGGCAACAAAGGAAACGGGTTTTG	1794
QY	567	PheLeuThrAsnAspTyrrPhePheThrAspIleSerAspThrProPheSerLeuGlyAla	586
Db	1795	GTGATGACAAATGACTACTATTATACAGACATCAAGGGTACTCTTTTCTAGTTTAGTGTC	1854
QY	587	ValLeuSerArgGlyHisGlyGluTyrrIleLeuLeuGlyLysAsnThrSerValGluGluGly	606
Db	1855	GGCTTTCCAGAGTTCATGGGAATATTTCTCCGAGGGAATGTAAACCATCGAAGAAGGC	1914
QY	607	LeuHisAspLeuLeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrrCysIleThr	626
Db	1915	CTGCATGACTTAGAACATCCGATGTCTCTTGGCAGATGAATGGTCTTACTGCAACACT	1974
QY	627	AspIleAspProAspHisArgLysLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThr	646
Db	1975	GACCTACACCTTGAGCAGCCCATCTGTCTCAGTTAGAACCGATTAAAGCTCTACCTAAAA	2034
QY	647	ArgLysAspProAspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAla	666
Db	2035	GGCAAGAAGACCTCTGCTCCAGTGTGNTAAGAAATTTGATCCAAGAGTCTCTTTTGACGC	2094
QY	667	ValValThrAlaProMetGluAlaTyrrTrpThrAlaLeuAlaLeuAsnMetSerGluGlu	686
Db	2095	GTGGTGAGTGCCTTGAAGCGTATTGGACAGCGCTGGCCCTCAACAAATCTGAAAAAT	2154
QY	687	SerGluHisValValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSer	706
Db	2155	TCGTGCAAGGGCGTGGAGGTTCCTTCGCGACTCGCACCGCGCTCTCCAGAAATCAAC	2214
QY	707	LeuPheValGlySerGluLysValSerAspArgLysPheLeuThrProGluAspGluAla	726
Db	2215	CTGTTTGTGGGGCTGAGCAGCTCACCATCAGGACTTCTCTGAAAGCTGGCGACAAGAG	2274
QY	727	SerValPheThrLeuAspArgPheProLeuTyrrArgGlnAlaSerGluHisProAla	746
Db	2275	AAACATTTTAAACGACAGACCATTTCCCTCTCTGTTACCGAAGAGCCGCTGACGAGATCCA	2334
QY	747	GlySerPheValPheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMet	766
Db	2335	GGGAGCTTCGTCTACTCGATCCCATTCAGCACTGGACCA-----GTCAATAAAGCAAT	2388
QY	767	ValValThrAlaSerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAla	786
Db	2389	GTGGTGACAGCAAGTACATCCATCCAGCTCCTGGATGAACGGAAATCTCTGTGGTGGCA	2448
QY	787	AlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaIleThrArg	806
Db	2449	GCTGTAGGCATTCAGATGAACCTTGAATTTTCCAAAGGAAGTCTCTGGACTGCGACAGA	2508
QY	807	GlnCysSerThrValAspGlyProTyrrThrGlnSerCysGluAspSerAspLeuAspCys	826
Db	2509	CAGTGTGCTTCCTCGATGGCAATGCTCCATCAGCTGTGATGATGAGACTGTGAAATGT	2568
QY	827	PheValIleAspAsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArg	846
Db	2569	TACCTCATAGACAATAATGATTTATTTTGGTGTCTGAAGACTTACACACAGACTGGAGAC	2628
QY	847	PheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSer	866
Db	2629	TTTTTGTGTGAGTACGAGGAGCTGTGATGAACAAATTTCTAACAAATGGGCTCTTTTAA	2688
QY	867	GlnValThrMetTyrrAspTyrrGlnAlaMetCysLysProSerSerHisHisSerAla	886
Db	2689	AGATTTACCTTTATGACTTACCAACCATGTGTAGCCCAACAGCAAGAAAGACGATGGC	2748
QY	887	AlaGlnProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGln	906


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Db 2749 GCCCATGCTCTCGGATCTTATAATGACCTTCTCTCGCAGTAAATGATCATGACA 2808
Qy 907 GluLeuValLeuPheLeuLeuGluTrpSerValTrpGlySerValTrpGlyArgGlyAla 926
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Qy 927 GluAlaLysSerValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnPro 946
Db 2866 ACAGCTAAAGCC-----CAGAAATTGAAACAGACCCCTGGAGCCT 2904
Qy 947 CysAspThrGluTrpProValPheValTrpGlnProAlaLeuArgGluAlaAsnGlyLe 966
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Qy 1047 GlyTrpAlaGlyPheSerSerProAsnPro 1056
Db 3199 TG-TGGGGTGGCGCGAGTCTCCAAGCCCA 3227
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RESULT 12

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US-10-162-102-16
; Sequence 16, Application US/10162102
; Publication No. US2003023236A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
; FILE REFERENCE: 10448-190001
; CURRENT APPLICATION NUMBER: US/10/162,102
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/875,321
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18398
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,238
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,363
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18247
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/227,068
; PRIOR FILING DATE: 2000-08-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 3276
; TYPE: DNA
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; ORGANISM: Homo sapiens
US-10-162-102-16
Alignment Scores:
Pred. No.: 0 Length: 3276
Score: 3416.50 Matches: 628
Percent Similarity: 77.81% Conservative: 189
Best Local Similarity: 59.81% Mismatches: 212
Query Match: 59.67% Indels: 22
DB: 18 Gaps: 7

US-09-833-222a-10 (1-1090) x US-10-162-102-16 (1-3276)
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Db 124 GTGAAGCTCTGGGCGCTCGGCTTTTGGTGGGAGATAAAATCCATTCGTGCTAAGTACTCC 183
Qy 33 GlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysLysLeuGlu 52
Db 184 GGTTCACAGCTTCGCAAAAGAAATACAAGAGTATGAGAAAGACGTTGCCATAGAAGAA 243
Qy 53 ValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArg 72
Db 244 ATTGATGGCTCTCAACTGTTAAAGAGCTGGCAAGAACATGGAGAGATGTTTCACAAG 303
Qy 73 LysValGluAlaValGlnAsnLeuValGluAlaGluGluAlaAspLeuAsnHisGlu 92
Db 304 AAGCTCTGAGCGCTCAGGCGCTGCTGGTGGAGGCTGCAGAGAGACACACCTGAAACATGAA 363
Qy 93 PheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuLeuLeuLeuLeuLeuLeu 112
Db 364 TTTGATGCAGACTTACAGTATGAATACTTCAATGCTGCTGCTGATAAATGAAGGGAGCAA 423
Qy 113 LysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuLeuLeuLeuLeuLeuLeuLeu 132
Db 424 GACGGGAATTTTGGAGCTGGGGAAGGAATTCCTTAGCCCCCAATGACCATTTTAAT 483
Qy 133 AsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyrAsnLys 152
Db 484 AATTTGCTGTGAACATCATGCTTAAGTGACGCTCAAGTACCAAGTACCAACGACATGTACAACAA 543
Qy 153 AspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheValGlu 172
Db 544 GACCTCGCAATTCGAATGGGTTTATGGTCTGGAATCTCTAAACAAAGTTTTTGTAGAT 603
Qy 173 AsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePhe 192
Db 604 AACTTTGACCGTGACCCCATCTCTCATATGGCAGTACTTTTGGAGTGCAGAGGGCTTTTT 663
Qy 193 ArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPheAspCys 212
Db 664 AGCAGTATCCGGGGATTAAATGGGAACCCAGATGAGAAATGGAGTCAATTCCTTCGACTGC 723
Qy 213 ArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeuVal 232
Db 724 AGGAACCGAAAAATGGTACATCCAGGCGAGCAACTTCTCCGAAAGACGGTGGTCAATTTAGTT 783
Qy 233 AspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThrThr 252
Db 784 GAGCTCAGTGGCAGCATGAAGGACTCCGCTGACTATCGGAAGCAACAGTCTCATCC 843
Qy 253 IleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAspTyrVal 272
Db 844 ATTTTGGATACACTTGGGATGATGACTTCTTCAACATATAATTCCTTATATAGGAGCTT 903
Qy 273 HistTrpIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAsnAspGlu 292
Db 904 CACTATGTGAACCTTGGCTGGAATGGAACCTTTGGTGAAGCCCGCAGCAGCAACAAAGAG 963
Qy 293 HisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAspGlnAla 312
Db 964 CACTTCAGGAGCATCTGGACAAACTTTTCGCCAAAGGAATTCGAATGTTGGATATAGCT 1023
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Db	3145	AGAGGCGCCAGAAATCTTGTCAATGGCTTCATCCTGAG-----GAGAAATGCAAGGGAG	3198
Qy	1047	GlyTyrAlaGlyPheSerSerProAsnPro	1056
Db	3199	TG-TGGGGGTGCGCCGAGTCTCCAAGGCCA	3227

RESULT 13

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US-09-875-423-1
; Sequence 1, Application US/09875423
; Patent No. US20020081657A1
; GENERAL INFORMATION:
;
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: 21784, A NOVEL HUMAN CALCIUM CHANNEL
; FILE REFERENCE: 10448-059001
; CURRENT APPLICATION NUMBER: US/09/875,423
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3690
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29) ... (3301)
US-09-875-423-1

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Alignment Scores:	
Pred. No.:	0
Score:	3416.50
Percent Similarity:	77.81%
Best Local Similarity:	59.81%
Query Match:	59.67%
DB:	9
Length:	3690
Matches:	628
Conservative:	189
Mismatches:	212
Indels:	22
Gaps:	7

US-09-833-222A-10 (1-1090) x US-09-875-423-1 (1-3690)

Qy	13	ValLysLeuTrpAlaAspThrPheGlyAspLeuTyrAsnThrValThrLysTyrSer	32
Db	152	GTGAAGACTCTGGGCGCTTTTGGTGGGAGATAAAATCCATTCGTGCTAAGTACTCC	211
Qy	33	GlySerLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIleGluGlu	52
Db	212	GGTTCACGCTTCTGCAAAAGAAATACAAAGAGTATGAGAAAGCGTGGCATAGAGAA	271
Qy	53	ValAspGlyLeuGluLeuValIargLysPheSerGluAspMetGluAsnMetLeuArgArg	72
Db	272	ATTGATGGCGCTCCAACTCGTAAGAAGCTGGCAAGAACATGGAAGAGATGTTTCCAAG	331
Qy	73	LysValGluAlaValGluAsnLeuValGluAlaIaGluGluAlaAspLeuAsnHisGlu	92
Db	332	AGCTGAGCGCGCTCGCGGCTCTGGTGGAGGCTGCAGAAAGACACCTGAAACATGAA	391
Qy	93	PheAsnGluSerLeuValIphaAspTyrTyrAsnSerValLeuLeuAsnGluArgAspGlu	112
Db	392	TTTGATGCAGACTTACAGTATCAATCTTCATCTGCTGCTGATAAATGAAAGGGACAA	451
Qy	113	LysGlyAsnPheValGluGlyValaGluPheLeuLeuGluSerAsnAlaHisPheSer	132
Db	452	GACGGGAATTTTGGAGCTGGAAAGAAATTCATCTTAGCCCAATAGACCAATTTAAT	511
Qy	133	AsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyrAsnLys	152
Db	512	AAATTTGCGCTGTCAACATCAGCTAAGTGACGTCCTCAAGTACCAACGACATGTACAAACA	571
Qy	153	AspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheValGlu	172
Db	572	GACCCCTGCAAATTTGTCAATGGGGGTTATTGGTCTGAATCTCTAAACAAAGTTTTGTAGAT	631
Qy	173	AsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePhe	192

Db 1703 CTCTCTGAGTGGAGTGGGAGACCGAGATGACGTGTTCGAGAAATGCTATGGTGAATCGA 1762
Qy 547 GluThrGlyThrLeuSerMetAspValLysValProMetAspLysGlyLysArgValLeu 566
Db 1763 AAGACGGGAGTTCCTTCCATGGAGGTGAAGAAGACAGTGGACAAAGGAAACGGGTTTG 1822
Qy 567 PheLeuThrAsnAspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAla 586
Db 1823 GTGATGACAAATGACTACTATTATACAGACATCAAGGGTACTCTTTCAGTTTGGTGTG 1882
Qy 587 ValLeuSerArgGlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGly 606
Db 1883 GCGCTTTCCAGAGTTCATCGGAATATTTCTCCGAGGAATGTAAACCATCGAAGAAGGC 1942
Qy 607 LeuHisAspLeuLeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThr 626
Db 1943 CTCATGACTTTAGAACATCCGAGTGTCTTGGCAGATGAATGGTCCCTACTGCAACACT 2002
Qy 627 AspIleAspProAspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThr 646
Db 2003 GACCTACACCTGAGCACCGCCATCTCTCAGTTAGAGCGATTAAAGCTCTACCTAAAA 2062
Qy 647 ArgLysAspProAspLeuGluCysAspGluLeuValArgGluValLeuPheAspAla 666
Db 2063 GGCAAAAGAACCTCTGCTCCAGTGTGATAAGAAATTCATCCAAAGAGTCCTTTTTCACGG 2122
Qy 667 ValValThrAlaProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGlu 686
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Qy 687 SerGluHisValValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSer 706
Db 2183 TCTGACAAAGCGCTGGAGGTGCTTCCTCGGCACTCGCAGGGCTCTCCAGAAATCAAC 2242
Qy 707 LeuPheValGlySerGluLysValSerAspArgLysPheLeuThrProGluAspGluAla 726
Db 2243 CTGTTTGTGCGGGCTGAGCAGCTCAGCAATCAGGACTTCCTGAAAGCTGCGCAGACAGAG 2302
Qy 727 SerValPheThrLeuAspArgPheProLeuTyrTrpArgGlnAlaSerGluHisProAla 746
Db 2303 AACATTTTAAACGACACCAATTTCCCTCTCTGTGTACGAAAGACCCCTGAGCAGATCCA 2362
Qy 747 GlySerPheValPheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMet 766
Db 2363 GGGAGCTCTGCTACTCGATCCCATTCAGCAGCTGGACCA-----GTCAATAAAGCAAT 2416
Qy 767 ValValThrAlaSerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAla 786
Db 2417 GTGGTGACAGCAAGTACATCCATCCAGCTCCTGGATGAACGGAAATCTCTGTGTGGTGGCA 2476
Qy 787 AlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPheThrAlaAlaThrArg 806
Db 2477 GCTGTAGGCATTCAGATGAACATTTGAATTTTCCAAAGGAAGTTCTGGACTGCCAGACA 2536
Qy 807 GlnCysSerThrValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCys 826
Db 2537 CAGTGTCTCCCTGGATGGCAATGCTCCATCAGCTGTGATGATCAGACTGTGAATTC 2596
Qy 827 PheValIleAspAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArg 846
Db 2597 TACCTCATAGACAATAATGGATTATTTTGGTGTCTGAAAGACTTACACAGACTGGAGAC 2656
Qy 847 PheLeuGlyValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSer 866
Db 2657 TTTTGGTGAGATCAGGAGCTGTGATGAACAAATTCGTAACAAATGGGCTCCTTTAA 2716
Qy 867 GlnValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisSerAla 886
Db 2717 AGAATTAACCTTTATGACTACCAAGCATGTGTGAGACCAACAGAAAGACGCGATGCG 2776
Qy 887 AlaGlnProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuGln 906
Db 2777 GCCCATGGCTCTGATCCTTATAATGCTTCTCTGCAATAAATGGATCATGACA 2836

Qy 907 GluLeuValLeuPheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAla 926
Db 2837 GAACCTTGCTTGTCTCTGGTGAATTTAACCTCTGC---AGTTGGGCACACTCCGATATG 2893
Qy 927 GluAlaLysSerValPheHisSerHisLysHisLysLysGlnAspProLeuGlnPro 946
Db 2894 ACAGCTAAAGCC-----CAGAAATTGAACACAGACCCTGGAGCCT 2932
Qy 947 CysAspThrGluTyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIle 966
Db 2933 TGTGATACTGAATATCCAGCATTCGTCTGAGCGCACCATCAAGGAGACTACAGGGAAT 2992
Qy 967 ValGluCysGlyProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeu 986
Db 2993 ATTGCTTGAAGACTGCTCCAGTCTTGTATCCAGAAATCCCAAGCAGCAACCTG 3052
Qy 987 LeuLeuLeuValThrAspProThrCysAspCysSerIlePheProProValLeuGlnGlu 1006
Db 3053 TTCATGGTGTGGTGGACAGAGCTGCTCTGTGAATCTGTGCCCCCCTACCATGGCA 3112
Qy 1007 AlaThrGluValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeu 1026
Db 3113 CCCATTGAATCAGGTATAATGAATCCCTTAAAGTGTGAACGTCTAAAGGCCCAGAAATC 3172
Qy 1027 ArgArgArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspArg 1046
Db 3173 AGAAGGCGCCAGAAATCTTGTATGGTTCCTCATCTAG-----GAGAATGCAGGGAG 3226
Qy 1047 GlyTrpAlaGlyPheSerSerProAsnPro 1056
Db 3227 TG-TGGGGTGGCGGAGTCTCCAAGCCCA 3255
RESULT 14
US-10-162-012-14
; Sequence 14, Application US/10162012
; Publication No. US20030051660A1
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Rory A.J.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
; FILE REFERENCE: 10448-190001
; CURRENT APPLICATION NUMBER: US/10/162,012
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/875,321
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18398
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,238
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,363
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18247
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/227,068
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 09/928,530
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/25475
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: US 60/226,770
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/934,421
; PRIOR FILING DATE: 2001-08-21

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; PRIOR APPLICATION NUMBER: PCT/US01/26096
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/279,281
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 10/109,029
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: PCT/US02/09728
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/290,288
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US (not assigned)
; PRIOR FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 3690
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)...(3301)
US-10-162-012-14

Alignment Scores:
Pred. No.: 0 Length: 3690
Score: 3416.50 Matches: 628
Percent Similarity: 77.81% Conservative: 189
Best Local Similarity: 59.81% Mismatches: 212
Query Match: 59.67% Indels: 22
DB: 15 Gaps: 7

US-09-833-222A-10 (1-1090) x US-10-162-012-14 (1-3690)

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Db 152 GTGAGCTCTGGGCTCGGCTTTGGTGGGAGATAAAATCCATTGCTGCTAGTACTCC 211

Qy 33 GlySerLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysLysGluGlu 52
Db 212 GGTTCACGCTTCTGCAAAAGAAATACAAAGAGTATGAGAAAGACGTTGCCATAGAAGAA 271

Qy 53 ValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArg 72
Db 272 ATTGATGGCTTCAACTGGTAAAGAGCTGGCAAGAACATGGAAGAGATGTTTCAAG 331

Qy 73 LysValGluAlaValGlnAsnLeuValGluAlaGluAlaAspLeuAsnHisGlu 92
Db 332 AAGCTTGAGGCCGCTCAGGCGCTCTGGTGGAGCTGCGAAGAGACACACCTGAAACATGAA 391

Qy 93 PheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuLeuAsnGluArgAspGlu 112
Db 392 TTTGATGCAGACTTACAGTATGAATCTTCAATGCTGTGCTGATATAATGAAGGGACAAA 451

Qy 113 LysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPheSer 132
Db 452 GACGGGAATTTTGGAGCTGGGAAGGAATTCATCTTACCCCAATGACCAATTTTAAAT 511

Qy 133 AsnLeuProValAsnThrSerLysSerValGlnLeuProThrAsnValTyrAsnLys 152
Db 512 AATTTGGCTGTGAACATCAGTCTAAGTGAGCTCCAGTACCAAGAACATGTAACACAAA 571

Qy 153 AspProAspLysLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheValGlu 172
Db 572 GACCTTGCATTTGCAATGGGTTTATTGGTCTGAACTCTCTAAACAAAAGTTTGTAGAT 631

Qy 173 AsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePhe 192
Db 632 AACTTTGACCGTACCCCATCTCATATGAGCTACTTTTGGAGTGGCAAGGGCTTTTT 691

Qy 193 ArgIleTyrProGlyLysLysTyrTrpProAspGluAsnGlyValLysThrPheAspCys 212
Db 692 AGCAGTATCCGGGGATTAAATGGGAACCAAGATGAGNATGGAGTCAATGCTTTCGACTGC 751

213 ArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeuVal 232
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233 AspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThrThr 252
Db 812 GACGTGAGTGGCAGCATGAAGGACTCCGCTGCTACTATCCGGAAGCAACAGCTCTCATCC 871

253 IleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAspTyrVal 272
Db 872 ATTTTGGATACACTTGGGATGATGACTTCTTCAACATAAATTTGCTTATATAGGAGCTT 931

273 HisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAsnArgGlu 292
Db 932 CACTATGTGGAACTTTCCTGGAATGGAACTTTGGTCAAGCCGACAGGACAAACAAAGAG 991

293 HisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAspGlnAla 312
Db 992 CACTTTCAGGAGCATCTGGACAAACTTTTCGCCAAGAGAAATTTGGAATGTTGGATATAGCT 1051

313 LeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySerLeuCys 332
Db 1052 CTGAATGAGGCTTCAACATTTCTGAGTGATTTTCAACCCACACGCGACAAAGGATATCTGC 1111

333 AsnGlnAlaIleMetLeuLysSerAspGlyAlaValGluAspTyrGluProValPheGlu 352
Db 1112 AGTCAGGCCATCATGCTCACTAATGATGGGCGGTGGACACCTATGATACAAATTTTGCA 1171

353 LysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArgGluVal 372
Db 1172 AAATCAATTTGGCCAGATCGAAAGGTTGCGATCTTCACTACCTCATTTGACGAGAGGCT 1231

373 SerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThrGlnIle 392
Db 1232 GCGTTTTCAGACAACTCTAAAGTCGATGGCTGTGCCAACAAAGAGATTTTACCAGATC 1291

393 SerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSerArgPro 412
Db 1292 TCCACCTTGGCTGATGTCAGGAGAAATGTCATGGAATACCTTCACGCTGCTTAGCGGCC 1351

413 MetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSerLysLeu 432
Db 1352 AAGTCATCGACCAGAGCATGATGTTGGTGTGGACCGAGCTTACATTTGACGACTCTC 1411

433 LeuSerSerGlnAlaGlnSerLeuThr-----LeuLeuThrThrVal 446
Db 1412 -----CCTCAGGCACAAAAGCTGACTGATGATCAGGCGCCCTGCTGTGACCACTGTA 1465

447 AlaMetProValPheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyVal 466
Db 1466 GCCATGCTGTGTTTGTAGTAAAGCAGAACGAAACCCAGATCGAAGGGCATTTCTTCTGGGAGTG 1525

467 ValGlySerAspValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGly 486
Db 1526 GTTGGCACAGATGTCCTCAGTGAAGAACTTCTGAAGACCATCCCAATATAAAGATTAGGG 1585

487 ValHisGlyTyrAlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeu 506
Db 1586 ATTACGGTTATGCTTTTCAATCAATAATATGATATATCTGACGCACTCCGGAATC 1645

507 ArgProLeuTyrArgGluGlyLysLysLeuLysProLysAspProAsnTyrAsnSerValAsp 526
Db 1646 AGGCTGCTGTGCAAGAGAGGAAAAAG---CGAAGGAAAAACCTTAACATATATAGTACGTTGAC 1702

527 LeuSerGluValGluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArg 546
Db 1703 CTCTCTGAGGTGGAGTGGGAAGACCGAGATGACGCTGTTGAGAAATGCTATGTTGGTATCGA 1762

547 GluThrGlyThrLeuSerMetAspValLysValProMetAspLysGlyLysArgValLeu 566
Db 1763 AAGACGGGGAAGTTTTCATGAGGTGGAAGACAGACAGTGGCAACAAAGGAAACGGGTTTG 1822

567 PheLeuThrAsnAspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAla 586

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Db 1823 GTGATGACAAATGACTACTATTATACAGACATCAAGGGTACTCTCTTCAGTTTGGTGTG 1882
Qy 587 ValLeuSerArgGlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGly 606
Db 1883 GCGCTTTCCAGAGGTATGAGGAATATTTCTCCGAGGGAATGTAACTCAAGGAGGC 1942
Qy 607 LeuHisAspLeuLeuHisProAspLeuAlaGlyAspTyrIleTyrCysIleThr 626
Db 1943 CTGCATGACTTAGACATCCGATGTCTCTGGCAGATGAATGGTCTTACTGCAACT 2002
Qy 627 AspIleAspProAspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThr 646
Db 2003 GACCTACACCTGAGCACCCTCTCTCAGTTAGAGCGATTAACTCTACCTAAAA 2062
Qy 647 ArgLysAspProAspLeuGluCysAspGluGluValArgGluValLeuPheAspAla 666
Db 2063 GGCAAGAACCTCTGCTCCAGTGTGATAAGAAATTGATCCAAAGAGTCCTTTTGACGG 2122
Qy 667 ValValThrAlaProMetGluAlaTyrTyrThrAlaLeuAlaLeuAsnMetSerGluGlu 686
Db 2123 GTGGTGAAGTCCCTTGAAGCGTATTGGACCGCTGCGCTTCAACAAATCTGAAT 2182
Qy 687 SerGluHisValValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSer 706
Db 2183 TCTGACAAGGGCGTGGAGGTGCTTCTCGGCACCTCGCACGGCGCTCTCCAGAAATCAAC 2242
Qy 707 LeuPheValGlySerGluLysValSerAspArgLysPheLeuThrProGluAspGluAla 726
Db 2243 CTGTGTGTCGGGCTGAGCAGCTCACCAATCAGACTTCTGAAAGCTGGCGACAGAG 2302
Qy 727 SerValPheThrLeuAspArgPheProLeuTyrTyrArgGlnAlaSerGluHisProAla 746
Db 2303 AACATTTTAAACGACAGACATTTCCTCTCTGTGACGAAGAGCGCTGAGCAGATTCCA 2362
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Pred. No.: 0
Score: 3416.50
Length: 3690
Matches: 628
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Db 2993 ATTGCTTGTGAAGACTGCTCCAAGTCTTGTGTCATCAGCAATCCNAGCAGCAACCTG 3052
Qy 987 LeuLeuLeuValThrAspProThrCysAspCysSerIlePheProValLeuGlnGlu 1006
Db 3053 TTCACTGGTGTGTGACAGACGCTGCTCTGTGAATCTGTGCGCCCATCCCATGGCA 3112
Qy 1007 AlaThrGluValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeu 1026
Db 3113 CCCATTGAATCAGGTATTAATGAATCCCTTAAGTGTGAACGCTTAAAGGCCCAAGATC 3172
Qy 1027 ArgArgArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspArg 1046
Db 3173 AGAAGGCGCCAGAAATCTTGTCTATGGCTTCCATCTGAG-----GAGAAATGCAAGGAG 3226
Qy 1047 GlyTyrAlaGlyPheSerSerProAsnPro 1056
Db 3227 TG-TGGGGTGGCGCGAGTCTCCAAGCCCA 3255

RESULT 15
US-10-162-102-14
; Sequence 14, Application US/10162102
; Publication No. US2003023236A1
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Rory A.J.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
; FILE REFERENCE: 10448-190001
; CURRENT APPLICATION NUMBER: US/10/162,102
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/875,321
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18398
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,238
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,363
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18247
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/227,068
; PRIOR FILING DATE: 2000-08-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 3690
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29) ... (3301)
US-10-162-102-14

Alignment Scores: 0
Pred. No.: 3416.50
Score: 3690
Matches: 628
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; PRIOR APPLICATION NUMBER: US 60/226,770
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/934,421
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US01/26096
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/279,281
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 10/109,029
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: PCT/US02/09728
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/290,288
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US (not assigned)
; PRIOR FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 3276
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-162-012-16

Alignment Scores:
Pred. No.: 0 Length: 3276
Score: 3416.50 Matches: 628
Percent Similarity: 77.81% Conservative: 189
Best Local Similarity: 59.81% Mismatches: 212
Query Match: 59.67% Indels: 22
DB: 4 Gaps: 7

US-09-833-222A-10 (1-1090) x US-10-162-012-16 (1-3276)
QY 13 ValLysLeuTrpAlaAspThrPheGlyAspLeuTyrAsnThrValThrLysTyrSer 32
Db 124 GTAAAGCTCTGGGCGCTGGGCTTTTGGTGGGAGATAAAATCCATTCGTGCTAAAGTACTCC 183
QY 33 GlySerLeuLeuGlnLysTyrLysAspValGluSerSerLeuLysAlaGluGlu 52
Db 184 GGTTCAGCTTCTGCNAAAGAAATACAAAGATATGAGAAAGACGTGTGCATAGAAGAA 243
QY 53 ValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArg 72
Db 244 ATTGATGGCTCCAACTGGTAAAGAGCTGGCAAGAGCATGCGAAGAGATGTTTCACAAG 303
QY 73 LysValGluAlaValGlnAsnLeuValGluAlaGluAlaGluAlaAspLeuAsnHisGlu 92
Db 304 AAGTCTGAGGCCGTCAGCGCTCTGGTGGAGGCTGCAGAAAGACACACCTGAAACATGAA 363
QY 93 PheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuLeuAsnGluArgAspGlu 112
Db 364 TTTGATGCAGACTTACAGTATGAAATCTCAATGCTGTGCTGATAAATGAAGGGACAAA 423
QY 113 LysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPheSer 132
Db 424 GACGGGAAATTTTGGAGCTGGGAAAGGAATTCATCTTAGCCCCCAAAATGACCAATTTAAT 483
QY 133 AsnLeuProValAsnThrSerLysLeuSerValGlnLeuProThrAsnValTyrAsnLys 152
Db 484 AATTTGCCCTGTGAACATCAGCTTAAGTGAGCTCCAAAGTACCAACGAAACATGATCAACAA 543
QY 153 AspProAspLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheValGlu 172
Db 544 GACCCCTGCAATTGCAATGGGTTTATTTGGTCTGAATCTCTAAACAAAGTTTGTAGAT 603
QY 173 AsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePhe 192
Db 604 AACTTTGACCGGTGACCCCATCTCTCATATGCGCAGTACTTTGGAAGTGCAAGGGCTTTT 663
QY 193 ArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPheAspCys 212
Db 664 AGCAGTATCCCGGGGATTAATATGGGAACCAAGATGAGAAATGGAGTCAATTCCTTCGACTGC 723
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QY 213 ArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeuVal 232
Db 724 AGGAACCGAAATGGTACATCCAGGAGCAAACTTCCGAAAGACGTGGTCAATTTAGTT 783
QY 233 AspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThrThr 252
Db 784 GAGCTCAGTGGCAGCATGAAGAGCTCCGCTGACTATCGCGAAGCAACAGTCTCATCC 843
QY 253 IleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAspTyrVal 272
Db 844 ATTTTGGATACACTTGGGATGATGACTTCTTCAACATAATTCCTTATAATGAGGAGCTT 903
QY 273 HisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAsnArgGlu 292
Db 904 CACTATGTGAACCTTGCCTGAATGGAACCTTTGGTCAAGCCGACAGGACAAACAAGAG 963
QY 293 HisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAspGlnAla 312
Db 964 CACTTCAGGGAGCATCTGGACAAACTTTTCGCCCAAGGAATTCGAATGTTGGATATAGCT 1023
QY 313 LeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySerLeuCys 332
Db 1024 CTGAATGAGGCGCTTCAACATTCCTGAGTGATTTCAACACACACCGGACCAAGAGTATCTGC 1083
QY 333 AsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProValPheGlu 352
Db 1084 AGTCAGGCCCATCATGCTCATTAATCTGATGGGCGGTGGACACCTATATACATCTTTTGCA 1143
QY 353 LysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArgGluVal 372
Db 1144 AAATACAAATTGGCCAGATCGAAAGGTTTCGATCTTTCACATACCTCATTTGGACGAGAGCT 1203
QY 373 SerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThrGlnIle 392
Db 1204 GCGTTTGCAGACAATCTAAAGTGGATGGCTGTGCCAACAAAGATTTTATACCCAGATC 1263
QY 393 SerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSerArgPro 412
Db 1264 TCACCTTGCTGTGTGTCAGGAGAAATGTCATGGAATACCTTCACGTGTTAGCCGCGCC 1323
QY 413 MetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSerLysLeu 432
Db 1324 AAAAGTCATCGACGAGGAGCATGATGGTGTGGACCGAAGCTTACATTTGACAGCACTCTC 1383
QY 433 LeuSerSerGlnAlaGlnSerLeuThr-----LeuLeuThrThrVal 446
Db 1384 -----CCTCAGGCACAAAGCTGATGATGATCAGGCGCCCGCTCTGTATGACCACTGTA 1437
QY 447 AlaMetProValPheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyVal 466
Db 1438 GCCATGCGCTGTGTTAGTAAAGCAGAACCAACAGATCGAAGGCATTTCTTCTGGAGTG 1497
QY 467 ValGlySerAspValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGly 486
Db 1498 GTTGGCACAGATGTCCAGTGAAGAACTTCTGGAAGACCATCCCAAAATACAAGTTAGGG 1557
QY 487 ValHisGlyTyrAlaPheLeuAsnThrAsnAsnGlyTyrIleIleuSerHisProAspLeu 506
Db 1558 ATTTCAGGTTATGCTTTGCAATCAAAATAATGATATATCTGTACGATCCGGAACCTC 1617
QY 507 ArgProLeuTyrArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAsp 526
Db 1618 AGGCTGCTGTACGAAGAGGAAAAAAG---CGAAGGAAACCTTAATATAGTAGCGTTGAC 1674
QY 527 LeuSerGluValGluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArg 546
Db 1675 CTCTCTGAGGTGGAGGAGACCGGATGATGCTGTGAGAAATGCTATGTTGGTGAATCGA 1734
QY 547 GluThrGlyThrLeuSerMetAspValLysValProMetAspLysGlyValArgValLeu 566
Db 1735 AAAGCGGGAAGTTCATGAGGTGAAGAAAGACAGTGGACAAAGGGAACCGGGTTTGTG 1794
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; PRIOR APPLICATION NUMBER: PCT/US02/09728
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/290,288
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US (not assigned)
; PRIOR FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 3690
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)...(3301)
US-10-162-012-14

Alignment Scores:
Pred. No.: 0 Length: 3690
Score: 3416.50 Matches: 628
Percent Similarity: 77.81% Conservative: 189
Best Local Similarity: 59.81% Mismatches: 212
Query Match: 59.67% Indels: 22
DB: 4 Gaps: 7

US-09-833-222A-10 (1-1090) x US-10-162-012-14 (1-3690)

QY 13 ValLysLeuTrpAlaAspThrPheGlyAspLeuTyrAsnThrValThrLysTyrSer 32
DB 152 GTGAAGCTCTGGGCGCTTGGTGGGGAGATAAAATCCATTCGTGTAAGTACTCC 211
QY 33 GlySerLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysLysLeuGlu 52
DB 212 GGTTCACAGCTTCTGCAAGAAGAAATACAAAGATGATGAGAAAGACGTTGGCCATAGAGAA 271
QY 53 ValAspGlyLeuGluLeuValAlaArgLysPheSerGluAspMetGluAsnMetLeuLysArg 72
DB 272 ATTGATGGCCCTCCAACTGGTAAAGAGCTGGCAAGAAATGATGAGAGAGATGTTTCACAAG 331
QY 73 LysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsnHisGlu 92
DB 332 AGTCTGAGCGCTGACGGCGCTGTTGGTGGAGCTGCAGAGAAAGACACACCTGAAACATGAA 391
QY 93 PheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuLysLeuGluArgAspGlu 112
DB 392 TTTGATCGACACTTACAGTATGATCTCAATGCTGTGCTGATTAATGAAAGGGACAAA 451
QY 113 LysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPheSer 132
DB 452 GACGGGAATTTTGGAGCTGGGAAAGGAATTCATCTTAGCCCCCAATGACCACTTTTAAT 511
QY 133 AsnLeuProValAsnThrSerLysLeuSerValGlnLeuProThrAsnValTyrAsnLys 152
DB 512 AATTGGCTGTGAACATCAGCTTAAGTGACGTCCAAAGTCCAAAGACGATGTAACACAAA 571
QY 153 AspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheValGlu 172
DB 572 GACCTGCAATTTGCAATGGGTTTATGCTGTGAATCTCTAAACAAAGTTTGTAGAT 631
QY 173 AsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePhe 192
DB 632 AACTTTGACCGTACCCTCTCATATGGCAGTACTTTGGAAGTGCMAAGGGGCTTTT 691
QY 193 ArgIleTyrProGlyIleLysTyrProAspGluAsnGlyValIleThrPheAspCys 212
DB 692 AGGACGATATCCGGGATTAATGGGAACCAAGATGAGAAATGGATGCTATTCCTTCGACTGC 751
QY 213 ArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeuVal 232
DB 752 AGNACCGAAATGGTATACATCCAGGACGAACTTCTCCGAAAGACGTTGCTATTTAGTT 811
QY 233 AspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThr 252
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Qy 607 LeuHisAspLeuLeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThr 626
Db 1943 CTGCATGACTTAGAACATCCGATGTCTCTTGGCAGATGAATGGTCTACTGCAACACT 2002
Qy 627 AspIleAspProAspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThr 646
Db 2003 GACCTACACCTTGAGCACCAGCCATCTGTCTCAGTTAAGAGCGATTAAAGCTCTACTTAAA 2062
Qy 647 ArgLysAspProAspLeuGluCysAspGluLeuValArgGluValLeuPheAspAla 666
Db 2063 GGCAAGAACCTCTGCTCCAGTGTATTAAGAATGTATCCAAAGAGTCCCTTTTGACGGC 2122
Qy 667 ValValThrAlaProMetGluAlaTyrTrpThrAlaLeuAlaLeuAlaLeuMetSerGluGlu 686
Db 2123 GTGGTGAAGTCCGCCATTAAGCGCTATTGGACCAAGCTGGCCCTCAACAAATCTGAAAT 2182
Qy 687 SerGluHisValValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSer 706
Db 2183 TCTGACAAAGGCGTGGAGGTTCCTCTCGGCACCTCGCAGGGCCCTCTCAGAAATCAAC 2242
Qy 707 LeuPheValGlySerGluLysValSerAspArgLysPheLeuThrProGluAspGluAla 726
Db 2243 CTGTTGTGGGGCTGAGCAGCTCACCANTCAGACCTTCTGAAAGCTGGCGCAAGGAG 2302
Qy 727 SerValPheThrLeuAspArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAla 746
Db 2303 AACATTTTAAACGCAGACCATTTCTCTCTGTGTACCGAAGAGCGCTGAGCAGATTCCA 2362
Qy 747 GlySerPheValPheAsnLeuArgTrpAlaGluClyProGluSerAlaGlyGluProMet 766
Db 2363 GGGAGCTTCGTCTACTCGATCCCATTCAGCACTGGACCA-----GTCAATAAAGCAAT 2416
Qy 767 ValValThrAlaSerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAla 786
Db 2417 GTGGTGACAGCAAGTACATCATCCAGCTCTGTGATGAAGCAAAATCTCTGTGGTGCA 2476
Qy 787 AlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArg 806
Db 2477 GCTGTAGGCATTACAGATGAATTTGAATTTTTCACAAAGGAAGTTCTGCACTGCCAGCAGA 2536
Qy 807 GlnCysSerThrValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCys 826
Db 2537 CAGTGTCTCTCCCTGGATGCCAAATGCTCCATCAGCTGTGTATGATGAGACTGTGAATGT 2596
Qy 827 PheValIleAspAsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArg 846
Db 2597 TACCTCATAGCAATAATAGATTTATTTTGGTGTCTGAGACTACACAGACTGGAGAC 2656
Qy 847 PheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSer 866
Db 2657 TTTTGTGGTGGATCGAGGAGCTGTGATGAACAAATTTGCTAACAAATGGGCTCTTTTAA 2716
Qy 867 GlnValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisSerAla 886
Db 2717 AGAATTCCTTTATGATCATCAACAGCATGTGTAGAGCCCAACAGAAAGACGCGATGGC 2776
Qy 887 AlaGlnProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGln 906
Db 2777 GCCCATGGCTCTCCGGATCCTTATATAGCCCTTCTCTCTGAGTAAATGGATCATGACA 2836
Qy 907 GluLeuValLeuPheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAla 926
Db 2837 GAACCTGTCTTGTCTGTGGTGAATTTAACTCTGC---AGTTGGTGGCCTCCGATATG 2893
Qy 927 GluAlaLysSerValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnPro 946
Db 2894 ACAGCTAAAGCC-----CAGAAATTGAACACAGACCTGGAGCCT 2932
Qy 947 CysAspThrGluTyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIle 966
Db 2933 TGTGATACTGNATATCCAGCATTCGTCTGTGAGCGCCACCATCAAGGAGACTACAGGGAAT 2992
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Qy 967 ValGluCysGlyProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeu 986
Db 2993 ATTGCTTGTGAAGACTGCTCCAAAGTCTTTTGTCTCCAGCAAAATCCCAAGCAGCAACTG 3052
Qy 987 LeuLeuLeuValThrAspProThrCysAspCysSerIlePheProProValLeuGlnGlu 1006
Db 3053 TTCTATGTGTGTGGACAGCACTGCTCTGTGAATCTCTGGCCCCCATCCACCATGGCA 3112
Qy 1007 AlaThrGluValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeu 1036
Db 3113 CCCATTGAATCAGGTATATGAATCCCTTAAGTGTGAACGTCTTAAAGGCCCAAGATC 3172
Qy 1027 ArgArgArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspArg 1046
Db 3173 AGAAGGCCCCAGATCTTGTCTATGGCTTCCATCTCTAG-----GAGAAATGCAAGGAG 3226
Qy 1047 GlyTrpAlaGlyPheSerSerProAsnPro 1056
Db 3227 TG-TGGGGTGGCCGAGTCTCCAAGCCCA 3255

RESULT 3
US-09-397-550-21
; Sequence 21, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-397-550-21

Alignment Scores:
Pred. No.: 0 Length: 3770
Score: 3410.50 Matches: 624
Percent Similarity: 77.87% Conservative: 189
Best Local Similarity: 59.77% Mismatches: 216
Query Match: 59.56% Indels: 16
DB: 4 Gaps: 6

US-09-833-222A-10 (1-1090) x US-09-397-550-21 (1-3770)
Qy 13 ValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLysTyrSer 32
Db 267 GTCAAGCTCTGGCCCTCGGCTTTTGGTGGGAGATAAAATCCATTCCTGCTAGTACTCC 326
Qy 33 GlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIleGluGlu 52
Db 327 GGTTCCAGCTTCTGCAAAAGAAATACAAAGAGATATGAGAAAGACGTTGCCATAGAAGAA 386
Qy 53 ValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArg 72
Db 387 ATTGATGGCCCTCCACTGTGTAAAGAGCTGGCAAGAACATGGAGAGATGTTTCACAG 446
Qy 73 LysValGluAlaValGlnAsnLeuValGluAlaGluGluAlaAspLeuAsnHisGlu 92
Db 447 AAGTCTGAGGCCCTCAGGCGTCTGGTGGAGCTGCAGAGAGCTGCAGAGAACACACCTGAAACATGAA 506
Qy 93 PheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArgAspGlu 112
Db 507 TTTGATGCGACACTTACAGTATGAATACTTCAATGCTGTCTGATGAATAATGAAGAGGACAA 566
Qy 113 LysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPheSer 132
Db 567 GACGGGAATTTTTTGGAGCTGGGAAAGGAATTCATCTTAGCCCCCAATGACCATTTTAAAT 626
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Qy	133	AsnLeuProValAsnThrSerIleSerValGlnLeuProThrAsnValTyrAsnLys	152
Db	627	AATTGGCTGTGAACATCAGTCTAAGTGACGCTCCAAGTACCAACGAACATGTACACAAA	686
Qy	153	AspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheValGlu	172
Db	687	GACCTTGCAAATGTCAATGGGGTTTATTGGTCTGAATCTCTAAACAAGTTTGTGTAGT	746
Qy	173	AsnPheGlnAspAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePhe	192
Db	747	AACTTTGACCGTGACCCATCTCTCATATGGCAGTACTTTTGGAGTGCAGAGGGCTTTT	806
Qy	193	ArgIleTyrProGlyIleLysTyrTrpThrProAspGluAsnGlyValIleThrPheAspCys	212
Db	807	AGGCAGTATCCGGGATTAATATGGGAACACAGATCAGAATGGAGTCAITTCCTTCGACTGC	866
Qy	213	ArgAsnArgGlyTyrTyrIleGlnAlaAlaThrSerProIysAspIleValIleLeuVal	232
Db	867	AGGAACCGAAATGGTATCATCCAGCGACGAACCTTCGGAAGACGTGGTCAITTTAGTT	926
Qy	233	AspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThr	252
Db	927	GACGTCAGTGGCAGCATGAAGGACTCCGTCTGACTATCGGAAGCAACAGCTCTCATCC	986
Qy	253	IleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAspTyrVal	272
Db	987	ATTTTGGATACATCTGGGATGATGATCTCTTCAACATATTTGCTTATATGAGGAGCTT	1046
Qy	273	HisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAsnArgGlu	292
Db	1047	CACATATGGGAACCTTGCTCTGAATGGAACTTTTGGTGAAGCCGACAGCAACAAAGAG	1106
Qy	293	HisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAspGlnAla	312
Db	1107	CACTTCAAGGAGCATCTGGACAAACTTTTTCGCCAAAGAAATGGAAATGTGGATATAGCT	1166
Qy	313	LeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySerLeuCys	332
Db	1167	CTGAATGAGGCTTCAACATCTCAGTGATTTCAACACACGGGACCAAGAGATATCTGC	1226
Qy	333	AsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProValPheGlu	352
Db	1227	AGTCAGGCCATCATGCTCATAACTGATGGGCGGTGGACACCTATGATCAACATCTTTGCA	1286
Qy	353	LysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArgGluVal	372
Db	1287	AAATACAAATTTGGCCAGATCGAAAGGTTTCGATCTTCATCACTCATTTGACAGAGGCT	1346
Qy	373	SerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThrGlnIle	392
Db	1347	CGCTTTCGACGACATCTAAAGTGATGGCCCTGTGCCAACCAAGAGATTTTATCCAGATC	1406
Qy	393	SerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSerArgPro	412
Db	1407	TCCACCTTGGCTGATGTGCAGGAGAAATGTCATGGAATACCTTCACGTGCTTAGCGGCC	1466
Qy	413	MetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSerLysLeu	432
Db	1467	AAAGTCATCGACCAAGGACATGATGTGGTGTGGACCAAGGCTTACATTCAGCAGCACTCTG	1526
Qy	433	LeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProValPheSer	452
Db	1527	ACTGATGATCAGGGCCCC-----GTCTGATGACCACTGTAGCCATGCCTGTGTTTAGT	1580
Qy	453	LysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAspValAla	472
Db	1581	AAGCAGAACGAAACACGATCGAAGGGCATCTCTCTGGAGTGGTGGCACACAGATGCCCCA	1640
Qy	473	LeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyrAlaPhe	492
Db	1641	GTGAAGAAGACTCTGAAGAGCCATCCCAAAATACAAAGTTAGGGATTCACGGTTATGCCTTT	1700

Qy	493	LeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyrArgGlu	512
Db	1701	GCAATCACAATAATATGTRTATATCTGACGCAATCCCGAACTCAGGCTGCTGTACGAAGAA	1760
Qy	513	GlyIysIleuLeuSerProLysProAsnTyrAsnSerValAspLeuSerGluValGluTrp	532
Db	1761	GGAAAAAG--CGAAGGAAACCTAACTATAGTAGCGTTGACCTCTCTGAGGTGGAGTGG	1817
Qy	533	GluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThrLeuSer	552
Db	1818	GAAGACCGAGATGACGTGTTGAGAAATGCTATGGTGNATCGAAAGACGGGGAAGTTTTC	1877
Qy	553	MetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsnAspTyr	572
Db	1878	ATGGAGGTGAAGAAGACAGTGGACAAAGGAAACGGGTTTTTGGTGTATGACAAATGACTAC	1937
Qy	573	PhePheThrAspIleSerAspThrProPheSerIleuGlyAlaValLeuSerArgGlyHis	592
Db	1938	TATTATACACACATCAAGGGTACTCTCTTTCAGTTTATAGTGTGGCGCTTCCACAGGTGCT	1997
Qy	593	GlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeuLeuHis	612
Db	1998	GGGAAATATTCTTCGAGGGAATGTAACTCGAAGAGCGCTGATGACTTAGAACAT	2057
Qy	613	ProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspProAspHis	632
Db	2058	CCCGATGTGCTTGGCAGATGAATGGTCTACTGCAACACATGACCTACACCTGAGCAC	2117
Qy	633	ArgLysLeuSerGlnIleuGluAlaMetIleArgPheLeuThrArgLysAspProAspLeu	652
Db	2118	CGCATCTGCTCAGTTAGAGCGGATTAAGCTCTACTCTAAAGCGCAAGAACCTCTGCCTC	2177
Qy	653	GluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAlaProMet	672
Db	2178	CAGTGTGATAAAGATTGATCCAAGAGTCTCTTTTGACCGGTGTGTAGTGCCCCCATY	2237
Qy	673	GluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisValValAsp	692
Db	2238	GAAGCGTATTGGACACGCTGGCCCTCAACAATCTGAAAATTTCTCACAAGGCGGTGGAG	2297
Qy	693	MetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGlySerGlu	712
Db	2298	GTTGCGCTTCTCGGCATCGCACGGCGCTCTCCAGAAATCAACCTGTGTGTGCGGGCTGAG	2357
Qy	713	LysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeuAsp	732
Db	2358	CAGCTACCAATCAGGACTTCCTGAAAGCTGGCGCACAGGACAACATTTTAAACGCAGAC	2417
Qy	733	ArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheValPheAsn	752
Db	2418	CAITTTCCCTCTCTGTTACCGAAGAGCGGTGACAGATTCACAGGAGCTTCGTCTACTCG	2477
Qy	753	LeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAlaSerThr	772
Db	2478	ATCCATTACGACTCGACCA-----GTCAATAAAAGCAATGTGTGTGACAGCAAGTACA	2531
Qy	773	AlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaGlyValGlnMet	792
Db	2532	TCCATCCAGCTCTGGATGAACGGAATCTCTGTGGTGGCAGCTGTAGCATTTACAGATG	2591
Qy	793	LysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThrValAsp	812
Db	2592	AAACTTGAATTTTCCAAAGGAGTTCTGGACTGCCACAGACAGCTGCTCCCTGGAT	2651
Qy	813	GlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAspAsnAsn	832
Db	2652	GGCAAAATGCTCCATCAGCTGTGATGATGAGACTGTGAATTTGTACCTCATAGACAATAAT	2711
Qy	833	GlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGluValAsp	852
Db	2712	GGATTTATTGTTGTCTGAAGACTACACAGACCTGGAGACTTTTTTGGTGTAGATCGAG	2771
Qy	853	GlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMetTyrAsp	872

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Db 2772 GGAGCTGTGTGACAAATGGCTAACCAATGGCTCCCTTTAAAGAAATACCCCTTTATGAC 2831
Qy TyrlGlnAlaMetCysLysProSerHisHisSerAlaAlaGlnProLeuValSer 892
Db 2832 TACCAGCCATGTGTAGCCCAACAGAAAGCAGCGATGGCGCCATCGCTCTCGAT 2891
Qy ProLeSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValPheLeu 912
Db 2892 CCTATAATGCTTCTCTCTGAGTAAATGGATCATGACAGAACTTGCTTGTCTG 2951
Qy LeuGluTrpSerValTrpGlySerTrpTrpAspArgGlyAlaGluAlaLysSerValPhe 932
Db 2952 GTGGAATTTAACTCTGC---AGTGTGGGACCTCCGATATGACAGCTAAAGCC--- 3002
Qy HisHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTrpPro 952
Db 3003 -----CAGAAATTTGAAACAGACCCCTGGAGCTTGTGATCTGAATATCCA 3047
Qy 953 ValPheValTrpGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGlyProCys 972
Db 3048 GCATTGCTCTGAGCGCACCATCAAGGAGACTACAGGGAATATTGCTTGTGAAGACTGC 3107
Qy 973 GlnLysValPheValGlnGlnIleProAsnSerAsnLeuLeuLeuValThrAsp 992
Db 3108 TCCAAGTCCCTTGTGATCCAGCAATCCCAAGCAGCAACCTGTTTCATGGTGGTGGAC 3167
Qy 993 ProThrCysAspCysSerIlePheProValLeuGlnGlnAlaThrGluValLysTyr 1012
Db 3168 AGCAGTCCCTCTGTGATCTGTGGCCCCCATCACCATGGCACCCATTTGAATCAGGTAT 3227
Qy 1013 AsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArgProAspSer 1032
Db 3228 AATGAATCCCTTAAGTGTGAACGTCTAAAGGCCAGAAAGATCAGAGGCGCCAGAACTCT 3287
Qy 1033 CysHisAlaPheHisProGluValArgValGluAlaAspArgGlyTrpAlaGlyPheSer 1052
Db 3288 TGTATGGCTTCCATCTCTGAG-----GAGAAATGCAAGGAGGTG-TGGGGGTGCGCGAG 3340
Qy 1053 SerProAsnPro 1056
Db 3341 TCTCCAAGCCCA 3352
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RESULT 4

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US-09-397-550-9
; Sequence 9, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 3213
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-397-550-9
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Alignment Scores:

Pred. No.:	0	Length:	3213
Score:	3400.50	Matches:	620
Percent Similarity:	78.12%	Conservative:	187
Best Local Similarity:	60.02%	Mismatches:	207
Query Match:	59.39%	Indels:	19
DB:	4	Gaps:	6

US-09-833-222a-10 (1-1090) x US-09-397-550-9 (1-3213)

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Qy 13 ValLysLeuTrpAlaAspThrPheGlyAspLeuTyrAsnThrValThrLysTyrSer 32
Db 124 GTGAAGCTCTGGGCTCGGCTTTTGGTGGGAGATAAAATCCATTTGCTGCTAAGTACTCC 183
Qy 33 GlySerLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIleGluGlu 52
Db 184 GGTTCACAGCTTCTGCAAAAGAAATACAAAGAGTATGAGAAAGACGTTGGCATAGAAGA 243
Qy 53 ValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArg 72
Db 244 ATTAGTGGCTCCCACTGGTAAAGAGCTGGCAAAAGCATGGAAGAGATGTTTTCACAAG 303
Qy 73 LysValGluAlaValGlnAsnLeuValGluAlaGluAlaAspLeuAsnHisGlu 92
Db 304 AAGTCTGAGGCGCTGAGCGCTCTGGTGGAGGCTGCAGAAAGACACACATGAAACATGAA 363
Qy 93 PheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArgAspGlu 112
Db 364 TTTGATGCAGACTTACAGTATGAATACTTCAATGCTGTGCTGATTAATGAAGAGGACAAA 423
Qy 113 LysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPheSer 132
Db 424 GACGGGAATTTTGGAGCTGGGAAAGGAATTCATCTTAGCCCAATGACCATTTTAAT 483
Qy 133 AsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyrAsnLys 152
Db 484 AATTTGCTGTGAACATCAGCTTAAGTGAGCTCCAAAGTACCAACGAAACATGTATCAACAAA 543
Qy 153 AspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPheValGlu 172
Db 544 GACCTTGCAATTTGCAATGGGTTTATTTGCTGTAATCTCTTAAACAAAGTTTTTGTAGAT 603
Qy 173 AsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePhe 192
Db 604 AACTTTGACCGCTGACCCATCTCTCATATGCGAGTACTTTTGGAAAGTGCAGGAGGCTTTT 663
Qy 193 ArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPheAspCys 212
Db 664 AGCAGTATTCGGGGATTAATATGGGAAACAGAGTACAGAAATGGAGTCAATTTGCTTCGACTGC 723
Qy 213 ArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeuVal 232
Db 724 AGGAACGGAATGTTGATACATCCAGGCGAGCAACTTCTCCGAAGACGTTGGTTCATTTAGTT 783
Qy 233 AspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThrThr 252
Db 784 GACGTGAGTGGCAGCATGAAAGGACTCCGCTGCTGACTATCGGAAGCAACACAGTCTCATCC 843
Qy 253 IleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAspTyrVal 272
Db 844 ATTTTGGATACACTTGGGGATGATGACTTCTTCAACATAATTTGCTTATAATAGGAGCTT 903
Qy 273 HisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsnArgGlu 292
Db 904 CACTATGTGGAACCTTGCCTGAATGGAACCTTTGGTGCAGCCAGCAGGACAAACAAAGAG 963
Qy 293 HisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAspGlnAla 312
Db 964 CACTTACGGGAGCATCTGGACAAACTTTTCCCAAGGAATTTGGAATGTTGGATATAGCT 1023
Qy 313 LeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnLysLeuCys 332
Db 1024 CTGAATGAGGCTTCAACATTTCTGAGTGATTTTCAACCCACACCGGAGCAAGAGTATCTGC 1083
Qy 333 AsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProValPheGlu 352
Db 1084 AGTCAGGCCATCATGCTCACTAATGATGGGCGGTGGACACCTATGATACAAATCTTTGCA 1143
Qy 353 LysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArgGluVal 372
Db 1144 AAATACAAATTTGGCCAGATCGAAAGGTTGCGATCTTTCACATACCTCATTTGGACGAGGCT 1203
Qy 373 SerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThrGlnIle 392
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Db      1204  GCGTTTCAGACAATCTAAAGTGGATGGCTGTGCCAACAAGGATTTTATCCGAGATC 1263
Qy      393  SerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSerArgPro 412
Db      1264  TCCACCTTGGCTGATGTGTCAGGAGAAATGTTCATGAATACCTTCACGTGCTTAGCGGCC 1323
Qy      413  MetValIleAsnHisAspHisAspIleIleTrrThrGluAlaTyrMetAspSerLysLeu 432
Db      1324  AAAGTCATCAGCCAGGAGCATGATGGTGTGACCGAAGCTTACATTTGACAGACTCTG 1383
Qy      433  LeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProValPheSer 452
Db      1384  ACTGATGATCAGGCGCCCC-----GTCCCTGATGACCACCTGTAGCCATGCCTGTGTAGT 1437
Qy      453  LysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAspValAla 472
Db      1438  AAGCAGAACCAACCAAGATCGAAGGGCATTTCTTCTGGGAGTGGTTGGCAGCATGTCCCA 1497
Qy      473  LeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyrAlaPhe 492
Db      1498  GTGAAGAACTTCTGAAGACCATCCCAATACAGTTAGGGATTCACGGTTATGCGCTTT 1557
Qy      493  LeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyrArgGlu 512
Db      1558  GCAATCACAAAATAATGGRTATATCTCGACGCATCCGGAACTCAGGCTGCTGTACGAAGA 1617
Qy      513  GlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluValGluTyr 532
Db      1618  GGAATAAAG---CGAAGAAACCTTAACATATAGTACGCTGTGACCTCTCTGAGGTGGAGTGG 1674
Qy      533  GluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThrLeuSer 552
Db      1675  GAAGACCGAGATGACGTGTGTAGAAATGCTATGTGTAATCGAAGACCGGGGAAGTTTCC 1734
Qy      553  MetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsnAspTyr 572
Db      1735  ATGGAGGTGAAGAAGACAGTGGACAAAGGCAACGGGTTTTGGTGATGACAAATGACTAC 1794
Qy      573  PhePheThrAspLysSerAspThrProPheSerLeuGlyAlaValLeuSerArgGlyHis 592
Db      1795  TATTTATACAGACATCAAGGGTACTCTCTTTCAGTTTAGGTGTGGCGCTTTCACAGAGTCA 1854
Qy      593  GlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeuLeuHis 612
Db      1855  GGGAAATATTTCTCCGAGGGAATGTAAACCATCGAAGAGGCTGTGATGATTAAGACAT 1914
Qy      613  ProAspLeuAlaLeuAlaGlyAspTrrPileTyrCysIleThrAspIleAspProAspHis 632
Db      1915  CCGAGTGTGTCTTGGCAGATGAATGGTCTCTACTGCAACACTGACCTACACCCCTGAGCAC 1974
Qy      633  ArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspProAspLeu 652
Db      1975  CGGCATCTGTCTCAGTTAGAGCGGATTAAGCTCTACCTAAAGGCCAAAGAACCTCTGTCT 2034
Qy      653  GluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAlaProMet 672
Db      2035  CAGTGTGATAAGAAATGTATCCAAGAGTCTCTTTTGACCGGTGTGTAGTGTGCCCCATT 2094
Qy      673  GluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisValValAsp 692
Db      2095  GAAGCGTATTGGACCGACCTGGCCCTCAACAAATCTGAAAAATTTCTGACAAAGGGCGTGGAG 2154
Qy      693  MetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGlySerGlu 712
Db      2155  GTTGGCTTCTCGGCACCTCGACCGGGCTCTCCAGAAATCAACCTGTGTGTGGGGCTGAG 2214
Qy      713  LysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeuAsp 732
Db      2215  CAGCTCACCAATCAGGACTTCTCTGAAAGCTGGCACAAGGAGAACATTTTAAACGCAGAC 2274
Qy      733  ArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheValPheAsn 752
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Db      2275  CATTTCCCTCTCTGGTACCGAAGAGCGCTGAGCAGATTCACGGAGCTTCGTCTACTCG 2334
Qy      753  LeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAlaSerThr 772
Db      2335  ATCCCAATTCAGCACTCGACCA-----GTCAATAAAGCAATGTGGTGACAGAAGTACA 2398
Qy      773  AlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaAlaGlyValGlnMet 792
Db      2389  TCCATCCAGCTCTCGATGNAACGGAATCTCTGTGGTGCGACGTGTAGGCATTCAGATG 2448
Qy      793  LysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThrValAsp 812
Db      2449  AAACCTTGAATTTTCCAAAGGAAGTTCTGGACTCGCCAGCAGACAGTGTGCTCCCTGGAT 2508
Qy      813  GlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAspAsnAsn 832
Db      2509  GGCAATGTCTCCATCAGCTGTGATGATGAGACTGTGAATTTGTACCTCATAGACAATAAT 2568
Qy      833  GlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGluValAsp 852
Db      2569  GGATTTATTTTGGTGTCTGAAGACTACACAGACTGGAGACTTTTGTGTGAGATCGAG 2628
Qy      853  GlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMetTyrAsp 872
Db      2629  GGAGCTGTGATGAACAAATTTGCTTAAACAATGGGCTCCTTTAAAAAGAATTTACCTTTATGAC 2688
Qy      873  TyrGlnAlaMetCysLysProSerSerHisHisSerAlaAlaGlnProLeuValSer 892
Db      2689  TACCAAGCATGTGTAGAGCCAAACAAAGGAAGCAGCGATGGCGCCCATGGCCCTCTCGAT 2748
Qy      893  ProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeu 912
Db      2749  CCTTATAATGCTCTCTCTCTGAGTAAATGGATCATGACAGAACTTGTCTTGTTCCTG 2808
Qy      913  LeuGluTrpSerValTrpGlySerTrrPyrAspArgGlyAlaGluAlaLysSerValPhe 932
Db      2809  GTGGAATTTAAACCTCTGC---AGTTGTGGCACTCCGATATGACAGCTAAAGCC----- 2859
Qy      933  HisHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrPro 952
Db      2860  -----CAGAAATTTGAACACAGACCCCTGGAGCCTTGTGATCTGTAATATCCA 2904
Qy      953  ValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGlyProCys 972
Db      2905  GCATTCGTCTCTGAGCGCACCATCAAGGAGACTACAGGGAATATTGCTGTGGAAGACTGC 2964
Qy      973  GlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuValThrAsp 992
Db      2965  TCCAAGTCTCTTTGTCTATCCAGCAAAATCCCAAGCAGCAACCTGTTCATGTGGTGGTGAC 3024
Qy      993  ProThrCysAspCysSerIlePheProProValLeuGlnGluAlaThrGluValLysTyr 1012
Db      3025  AGCAGTCTGCTCTGTGAATCTGTGGCCCCCATCACCATGGCACCCTTTGAAATCAGGTAT 3084
Qy      1013  AsnAlaSerValLysCysAspArgMet-----ArgSerGlnLysLeu 1026
Db      3085  AATGAATCCCTTAAGTGTGAACGTCTAAAGGCCCCAGCAAGATCAGAAGGCCCAAGAAGATC 3144
Qy      1027  ArgArgArgProAspSerCysHisAlaPheHisProGlu 1039
Db      3145  AGAAGCGGCCCAAGAATCTTTGTCTATGGCTTCCATCTCTGAG 3183

RESULT 5
US-09-397-550-8
; Sequence 8, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
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; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 3114
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-397-550-8

Alignment Scores:
Pred. No.: 0 Length: 3114
Score: 3326.50 Matches: 606
Percent Similarity: 78.32% Conservative: 185
Best Local Similarity: 60.00% Mismatches: 206
Query Match: 58.09% Indels: 13
DB: 5 Gaps: 4

US-09-833-222A-10 (1-1090) x US-09-397-550-8 (1-3114)

Qy 13 ValLysLeuTrpAlaAspThrPheGlyAspLeuTyrAenThrValThrLysTyrSer 32
Db 124 GTGAAGCTCTGGGCTCGGCTTTGGTGGGAGATAAAATCCATTGCTGCTAAGTACTCC 183

Qy 33 GlySerLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysLysGluGlu 52
Db 184 GGTTCAGCTTCTGCAAAAGAAATACAAAGAGTATGAGAAAGACGTTGCCATAGAGAA 243

Qy 53 ValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAenMetLeuArgArg 72
Db 244 ATTGATGGCTTCCAACTGGTAAAGAACTGCGAAAGAACATGGAAAGAGATGTTTCACAG 303

Qy 73 LysValGluAlaValGlnAenLeuValGluAlaGluAlaAspLeuAenHisGlu 92
Db 304 AAGTCTGAGGCGCTGAGGCGTCTGGTGGAGCTGCAGAGAGACACACCTGAAACATGAA 363

Qy 93 PheAenGluSerLeuValPheAspTyrTyrAenSerValLeuLeuAenGluArgAspGlu 112
Db 364 TTTGATGCAGACTTACAGTATGATCTTCAATGCTGTGCTGATAAATGAAGGGACAA 423

Qy 113 LysGlyAenPheValGluLeuGlyValGluPheLeuLeuGluSerAenAlaHisPheSer 132
Db 424 GACGGGAATTTTTGGAGCTGGGAAGGAATTCATCTTACGCCCAATGACCATTTTAA 483

Qy 133 AenLeuProValAenThrSerIleSerSerValGlnLeuLeuProThrAenValTyrAenLys 152
Db 484 AATTGGCTGTGAACATCAGTCTAAGTGACGTCCAGTACCAACGAAACATGTACAAACA 543

Qy 153 AspProAspIleLeuAenGlyValTyrMetSerGluAlaLeuAenAlaValPheValGlu 172
Db 544 GACCTGCAATTTGTCAATGGGGTTTATTGGTCTGAAATCTCTAAACAAAGTTTTGTAGAT 603

Qy 173 AenPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePhe 192
Db 604 AACTTTGACCGTGACCATCTCTCATATGGCAGTACTTTGGAAGTGCAGAGGGCTTTTT 663

Qy 193 ArgIleTyrProGlyIleLysTrpThrProAspGluAenGlyValIleThrPheAspCys 212
Db 664 AGCAGTATCCGGGATTAATGGGAACCATGAGATGAGATGAGTCAATTCGCTTCGACTGC 723

Qy 213 ArgAenArgGlyTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeuVal 232
Db 724 AGGAACCGAAATGGTATACATCCAGGCAGCACTTCTCCGAAAGACGTTGCTTATAGTT 783

Qy 233 AspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThrThr 252
Db 784 GACCTAGTGACATGAAAGGACTCCGCTGACTACTCGGAAGCAACAGCTCTCACTCC 843

Qy 253 IleLeuAspThrLeuGlyGluAenAspPheValAenIleIleAlaTyrAenAspTyrVal 272
Db 844 ATTTTGGATACACTTGGGATGATGACTTCTTCAACATTAATTCCTTATATAGAGACCT 903

Qy 273 HisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAenArgGlu 292
Db 903

Db 904 CACTATGTGGAACTTGGCTCGCTGAATGAACTTTGGTGCAGCCAGGACAAACAAAGAG 963

Qy 293 HisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAspGlnAla 312
Db 964 CACTTCAGGAGCATCTGGACAAACTTTTCGCCAAAGGAATTTGGAATTTGGATATAGCT 1023

Qy 313 LeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySerLeuCys 332
Db 1024 CTGAATGAGGCTTCAACATTTCTGAGTGAATTTCAACCCACACCGGACAAAGAGTATCTGC 1083

Qy 333 AenGlnAlaIleMetLeuIleSerAspGlyValAlaValAspTyrGluProValPheGlu 352
Db 1084 AGTCAGCCCATCATGCTCATACTGATGGGCGGTGACACCTATGATACAACTTTTGCA 1143

Qy 353 LysTyrAenTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArgGluVal 372
Db 1144 AATACAAATTTGGCCAGATCGAAAGTTTCGATCTTCACATACCTCATTGGACGAGGCT 1203

Qy 373 SerPheAlaAspArgMetLysTrpIleAlaCysAenAenLysGlyTyrTyrThrGlnIle 392
Db 1204 GCGTTTGCAGACAATCTAAAGTGGATGGCGCTGTGCCAAACAAAGGATTTTATCCGACATC 1263

Qy 393 SerThrLeuAlaAspThrGlnGluAenValMetGluTyrLeuHisValLeuSerArgPro 412
Db 1264 TCCACCTTGGCTGATGTGCAGGAGATGCTCATGGAATACCTTCACGTGCTTAGCCGCC 1323

Qy 413 MetValIleAenHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSerLysLeu 432
Db 1324 AAGTCATCGACAGGAGCATGATGGTGGACCGAAGCTTACATTTGACAGACACTGTG 1383

Qy 433 LeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrValAlaMetProValPheSer 452
Db 1384 ACTGATGATCAGGCGCCCTCTCTCTGATGACCATCTAGCCATGCTGTGTGTAGT 1437

Qy 453 LysLysAenGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAspValAla 472
Db 1438 AAGCAACGAAACCAAGATCGAAGGGCATCTCTCTGGAGTGGTGGCAGATGTGCCA 1497

Qy 473 LeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyrAlaPhe 492
Db 1498 GTGAAGAACTTCTGAAGACCATCCCAATACAAAGTTAGGATTCACGGTTATGCTTT 1557

Qy 493 LeuAenThrAenAenGlyTyrIleLeuSerHisProAspLeuArgProLeuTyrArgGlu 512
Db 1558 GCAATCACAAATTAATGRTATATCTTCGACGCATCCGGAACCTAGGCTGTACGAAGAA 1617

Qy 513 GlyLysLysLeuLysProLysProAenTyrAenSerValAspLeuSerGluValGluTrp 532
Db 1618 GGAAGAAAG---CGAAGGAACCTTAATATAGTGGCTTGACCTCTCTGAGTGGAGTGG 1674

Qy 533 GluAspGlnAlaGluSerLeuArgThrAlaMetIleAenArgGluThrGlyThrLeuSer 552
Db 1675 GAAGACCGAGATGACGTGTTGGAATGCTATGTAATCGAAGACGCGGGAAGTTTTC 1734

Qy 553 MetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAenAspTyr 572
Db 1735 ATGGAGGTGAAGAGACAGTGGACAAAGGGAACCGGTTTGTGTGATGACAAATGACTAC 1794

Qy 573 PhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArgGlyHis 592
Db 1795 TATTATACAGCATCAAGGGTACTCTCTTTCAGTTTAGTGGCTTTTCAGAGGTTCAT 1854

Qy 593 GlyGluTyrIleLeuLeuGlyAenThrSerValGluGlyLeuHisAspLeuLeuHis 612
Db 1855 GGAATATATTTCTCCGAGGGAATGTAACCATCGAAGAGGCTGCTGATGACTTAGAACAT 1914

Qy 613 ProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspProAspHis 632
Db 1915 CCCGATGTGTCTTGGCAGATGAATGGTCTCTACTGCAACACTGACCTACACCTTGAGCAC 1974

Qy 633 ArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspProAspLeu 652
Db 1975 CGCCATCTGTCTCAGTTAGAACGATTAAGCTCTTACCTTAAAGGCAAGAACCTCTGCTC 2034

Qy	653	GluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAlaProMet	672
Db	2035	CAGTGTGATAAAGAATTGATCCAAGAAGTCCTTTTTCAGCGGTGTGTGAGTGCCGCCCAT	2094
Qy	673	GluAlaTyrTrpThrAlaLeuAlaIleAsnMetSerGluGluSerGluHisValValAsp	692
Db	2095	GAAGCGTATTGGACGAGCTGGCCCTCAACAAATCTGAAATCTGCAAGGGCGGTGGAG	2154
Qy	693	MetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGlySerGlu	712
Db	2155	GTTGCCCTCTCGGCATCTCGACCGGCTCTCCAGAATCAACCTGTGTGTGGGGCTGAG	2214
Qy	713	LysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeuAsp	732
Db	2215	CAGCTCACCAATCAGGACTTCTGAAAGCTGGCGACAGGAGAACATTTTAAACGCAGAC	2274
Qy	733	ArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheValPheAsn	752
Db	2275	CATTTCCTCTCTGGTACCGAAGACCGCTGAGCAGATTCACAGGAGCTTCTGTCTACTCG	2334
Qy	753	LeuArgTrpAlaGluGlyProGluSerAlaGlyLeuProMetValValThrAlaSerThr	772
Db	2335	ATCCCATTCAGACTGGACCA-----GTCAAATAAAGCAATGTGGTGACAGCAAGTACA	2388
Qy	773	AlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaGlyValGlnMet	792
Db	2389	TCCATCAGCTCCTGGATGAACGAAATCTCCTGTGTGGCAGCTGTAGCAATTCAGATG	2448
Qy	793	LysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThrValAsp	812
Db	2449	AACTTGAATTTTTCCAAAGAAATTTCTGGACTCCACAGACACAGTGTGCTTCCTGGAT	2508
Qy	813	GlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAspAsnAsn	832
Db	2509	GGCAAAATGCTCCATCAGCTGTGATGATGAGACTGTGAATTTGTACCTCATAGACAAATAT	2568
Qy	833	GlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGluValAsp	852
Db	2569	GGATTTATTTGGTGTCTGAAGACTACACAGACTCGAGACTTTTGTGTGAGATCGAG	2628
Qy	853	GlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMetTyrAsp	872
Db	2629	GGAGCTGTGATGAACAAATTCGTAAACATGGGCTCCTTTAAAGAAATTAACCTTTATGAC	2688
Qy	873	TyrGlnAlaMetCysLysProSerSerHisHisSerAlaAlaGlnProLeuValSer	892
Db	2689	TACCAAGCCATGTGTAGAGCCAAACAGGAAGCAGCGATCGCGCCCATGCCCTCTGGAT	2748
Qy	893	ProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeu	912
Db	2749	CCATTATATGGCTTCCTCTCTGCGAGTAAATGGATCATGACAGACTTGTCTGTCTCTG	2808
Qy	913	LeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSerValPhe	932
Db	2809	GTGGAAATTTAAACCTCTGC-----AGTTGTGGCAGCTCCGATATGACAGCTAAAGCC	2859
Qy	933	HisHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrPro	952
Db	2860	-----CAGAAATTTGAAACAGACACCCCTGGAGCCTTGTGATACTGAATATCCA	2904
Qy	953	ValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGlyProCys	972
Db	2905	GCATTCTCTCTGAGCCGCCACCATCAAGAGACTACAGGGAATATTTGCTGTGAAGACTGC	2964
Qy	973	GlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuValThrAsp	992
Db	2965	TCCAAGTCTTTGTTCATCCAGCAATCCCAAGCAGCAACCTGTTTCATGGGTGGTGGAC	3024
Qy	993	ProThrCysAspCysSerIlePheProValLeuGlnGluAlaThrGluValLysTyr	1012
Db	3025	AGCAGCTGCTGTGTGAATCTGTGGGCCCATCATCACCATTGGCACCACCATTTGAATCAGGTAT	3084

QY	1013	AsnAlaSerValLysCysAspArgMetArg	1022
Db	3085	AATGAATCCCTTAAGTGTGAACGCTCTAAAG	3114
RESULT 6			
US-09-397-550-7			
; Sequence 7, Application US/09397550			
; Patent No. 6783952			
; GENERAL INFORMATION:			
; APPLICANT: Warner-Lambert			
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2			
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and			
; TITLE OF INVENTION: screening assays using same			
; FILE REFERENCE: 180			
; CURRENT APPLICATION NUMBER: US/09/397,550			
; CURRENT FILING DATE: 1999-09-16			
; NUMBER OF SEQ ID NOS: 28			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 7			
; LENGTH: 3057			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-09-397-550-7			
Alignment Scores:			
Pred. No.:	0	Length:	3057
Score:	3278.50	Matches:	599
Percent Similarity:	78.51%	Conservative:	179
Best Local Similarity:	60.44%	Mismatches:	200
Query Match:	57.26%	Indels:	13
DB:	4	Gaps:	5
US-09-833-222A-10 (1-1090) x US-09-397-550-7 (1-3057)			
QY	13	ValLysLeuTrpAlaAspThrPheGlyAspLeuTyrAsnThrValThrLysTyrSer	32
Db	124	GTGAAGCTCTGGGCGCTCGGCTTTTGGTGGGAGATATAAATCCATTCTGCTAAGTACTCC	183
QY	33	GlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIleGluGlu	52
Db	184	GGTTCCAGCTTCTGCANAAGAANAATCAAGAGATGTAGAAGACGCTGCCATAGAAGAA	243
QY	53	ValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArg	72
Db	244	ATTGATGGCTCCCAACTGGTAAAGAAGCTGGCAAGAACATGGAAGAGATGTTTCACAAG	303
QY	73	LysValGluAlaValGlnAsnLeuValGluAlaLysGluAlaAspLeuAsnHisGlu	92
Db	304	AAAGTCTGAGCGCGTCTGGTGGAGCGTGCAGAGAAGACACACCTGAAACATGAA	363
QY	93	PheAsnGluSerLeuValPheAspTyrTyrAsnSerValIleAsnGluArgAspGlu	112
Db	364	TTTGATGCAGACTTACAGTATGAATAACTCAATGCTGCTGATAAATGAAAGGGACAA	423
QY	113	LysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHisPheSer	132
Db	424	GACGGGAATTTTGGAGCTGGGAAGGAATTCATCTTAGCCCCAANTGACCATTTAAT	483
QY	133	AsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyrAsnLys	152
Db	484	AAATTGGCTGTGAACATCAGTCTAAGTGACGCTCCAAGTACCAACGAACATGTACAA	543
QY	153	AspProAspIleLeuAsnGlyValTyrMetSerGluAlaIleAsnAlaValPheValGlu	172
Db	544	GACCTGTCAATGTCAATGGGGTTTATGGTGTGAATCTCTAAACAAGATTTTGTAGAT	603
QY	173	AsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePhe	192
Db	604	AACTTTGACCGTGACCCATCTCTCATATGGCAGTACTTTGGGAAGTGCAAAGGCTTTT	663
QY	193	ArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPheAspCys	212
Db	664	AGGCAGTATCCGGGATTAATCGGAACACAGATGAGATGGAGTCAATTCGCTTCGACTGC	723


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Db 2860 -----CAGAAATTGAAACACAGACCCCTGGAGCTTGTGATCTGATATCCA 2904
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Qy 953 ValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGlyProCys 972
      |||:::
      |||:::
Db 2905 GCATTCTCTGAGCGCACCATCAGGAGACTACAGGGAATATTGCTTGAAGACTGC 2964
      |||:::
      |||:::
Qy 973 GlnLysValPheValGlnGlnIleProAsnSerAsnLeuLeuLeuValThrAsp 992
      |||:::
      |||:::
Db 2965 TCCAAAGTCTTGTATCCAGCAAAATCCCAAGCAGCAACCTGTTCAATGGTGGTGGAC 3024
      |||:::
      |||:::
Qy 993 ProThrCysAspCysSerIlePheProVal 1003
      |||:::
      |||:::
Db 3025 AGCAGCTGCCTCTGTGAATCTGTGGCCCCCATC 3057
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RESULT 7
US-09-397-550-15
; Sequence 15, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 15
; LENGTH: 1050
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-397-550-15
Alignment Scores:
Pred. No.: 4,77e-195 Length: 1050
Score: 1792.50 Matches: 341
Percent Similarity: 98.00% Conservative: 2
Best Local Similarity: 97.43% Mismatches: 6
Query Match: 31.30% Indels: 1
DB: 4 Gaps: 1
US-09-833-222A-10 (1-1090) x US-09-397-550-15 (1-1050)
Qy 700 AlaGlyLeuLeuArgSerSerLeuPheValGlySerGluLysValSerAspArgLysPhe 719
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      ::|
Db 1 AGTGCCCTCTCTGAGAAGCAGCTTGTTCGTGGGCTCCGAGAAGTCTCCGACAGGAAGTTC 60
      |||
      |||
Qy 720 LeuThrProGluAspGluAlaSerValPheThrLeuAspArgPheProLeuTyrTyrArg 739
      |||
      |||
Db 61 CTGACACCTGAGACGACGACGCGGTTCACCTCGACCGCTTCGCGTGTGGTACCGC 120
      |||
      |||
Qy 740 GlnAlaSerGluHisProAlaGlySerPheValPheAsnLeuArgTrpAlaGluGlyPro 759
      |||
      |||
Db 121 CAGGCTCTCAGAGCATCTGCTGCGAGCTTCTTCAACCTCGCTGGCGCAGAAGACCA 180
      |||
      |||
Qy 760 GluSerAlaGlyGluProMetValValThrAlaSerThrAlaValAlaValThrValAsp 779
      |||
      |||
Db 181 GAAAGTGGGGTGAACCCATGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
      |||
      |||
Qy 780 LysArgThrAlaIleAlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArg 799
      |||
      |||
Db 241 AAGAGACACCAATTGCTGACGCGCGGGGCTCAAAATGAAGCTGGAATTCCTCCAGCGC 300
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      |||
Qy 800 LysPheTrpAlaAlaThrArgGlnCysSerThrValAspGlyProTyrThrGlnSerCys 819
      |||
      |||
Db 301 AAATTTCTGGCGCGCAACGCGCAGTGCAGCACTGTGATGGGCGGTGCACACAGAGCTGC 360
      |||
      |||
Qy 820 GluAspSerAspLeuAspCysPheValIleAspAsnGlyPheIleLeuIleSerLys 839
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      |||
Db 361 GAGGACAGTGATCTGACTGCTTCTCGTATCGACCAACAAACGGGTTCATTCTGATCTCCAAG 420
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Qy 840 ArgSerArgGluThrGlyArgPheLeuGlyGluValAspGlyAlaValLeuThrGlnLeu 859
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Db 421 AGTCCCGAGAGACGGAAGATTCTTGGGGAGGTGGATGGTCTGCTCTGACCCAGCTG 480
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      |||
Qy 860 LeuSerMetGlyValPheSerGlnValThrMetTyrAspTyrGlnAlaMetCysLysPro 879
      |||
      |||
Db 481 CTCAGCATGGGGTGTTCAGCCAAAGTGACTATGTATGACTATCAGGCCATGTGCAAAACC 540
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      |||
Qy 880 SerSerHisHisSerAlaAlaGlnProLeuValSerProIleSerAlaPheLeuThr 899
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      |||
Db 541 TCGAGTCACACACACAGTGCAGCCAGCCCTGGTCAGCCCAATTTCTGCCCTTCTTGACG 600
      |||
      |||
Qy 900 AlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLeuGluTyrPheValTyrGly 919
      |||
      |||
Db 601 GCGACCAAGTGTCTGCTGAGGAGCTGGTGTCTTCTGCTGGAGTGGAGTGTCTGGGGC 660
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      |||
Qy 920 SerTrpTyrAspArgGlyAlaGluAlaLysSerValPheHisSerHisLysLys 939
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      |||
Db 661 TCTGTGTACGACAGAGGGCGGAGGCAAAAGTGTCTTCATCATCTCCCAACACACAAG 720
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      |||
Qy 940 LysGlnAspProLeuGlnProCysAspThrGluTyrProValPheValTyrGlnProAla 959
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      |||
Db 721 AAGCAGGACCCCTGCAGCCCTGCGACACGAGTACCCCGTGTCTGTGTACCGCGGCC 780
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      |||
Qy 960 IleArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLysValPheValValGln 979
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Db 781 ATCCGGGAGGCCAACCGGATCTGTGGAGTGGGGCCCTGCCAGAGGATATTGTGTGTCAG 840
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      |||
Qy 980 GlnIleProAsnSerAsnLeuLeuLeuValThrAspProThrCysAspCysSerIle 999
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      |||
Db 841 CAGATTCCCAACAGTAACCTCTCTCTCTGTCGACAGACCCACCTGTGACTGCAGCATC 900
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      |||
Qy 1000 PheProValLeuGlnGluAlaThrGluValLysTyrAsnAlaSerValLysCysAsp 1019
      |||
      |||
Db 901 TTCCACCACTGCTGCGAGGAGCGACAGAAGTCAAAATAATATGCTCTGTCAAAATGTGAC 960
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      |||
Qy 1020 ArgMetArgSerGlnLysLeuArgArgProAspSerCysHisAlaPheHisProGlu 1039
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Db 961 CGGATGGCTCCAGAGAGTCCGCGGCGACAGACTCTCTGCCACGCCCTTCCATCCAGAG 1020
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Qy 1040 ValArgValGluAlaAspArgGlyTrpAla 1049
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Db 1021 GAGAAATGCCAG---GACTGCGCGCGGCC 1047
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RESULT 8
US-09-397-550-14
; Sequence 14, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-397-550-14
Alignment Scores:
Pred. No.: 6,27e-184 Length: 969
Score: 1695.00 Matches: 321
Percent Similarity: 99.69% Conservative: 1
Best Local Similarity: 99.38% Mismatches: 1
Query Match: 29.60% Indels: 0
DB: 4 Gaps: 0
US-09-833-222A-10 (1-1090) x US-09-397-550-14 (1-969)

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Qy 700 AlaGlyLeuLeuArgSerSerLeuPheValGlySerGluLysValSerAspArgLysPhe 719
Db 1 AGTGGCTCTCTGAGAACGAGCTGTTGCTGGCTCCGAGAGGTCTCCGACAGGAAGTTC 60
Qy 720 LeuThrProGluAspGluAlaSerValPheThrLeuAspArgPheProLeuTyrPyrArg 739
Db 61 CTGACACCTGAGGACGAGGCGAGCTGTTACCTCGGACCGCTTCCGCGTGTGGTACCGC 120
Qy 740 GluAlaSerGluHisProAlaGlySerPheValPheAsnLeuArgTTPAlaGluGlyPro 759
Db 121 CAGGCTCAGAGCATCTCTGTGCGAGCTTCTTCAACCTCGCTGGGCGGAGGACCA 180
Qy 760 GluSerAlaGlyGluProMetValThrAlaSerThrAlaValAlaValThrValAsp 779
Db 181 GAAAGTGGGCTGAACCCATGGTGTGACGCAAGCACAGCTGTGGCGGTGACCGTGGAC 240
Qy 780 LysArgThrAlaIleAlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArg 799
Db 241 AAGAGGACAGCCATTGCTGACGCGCGGCGCTCCAAATGAAGCTGGAATTTCTTCCAGCGC 300
Qy 800 LysPheTTPAlaAlaThrArgGlnCysSerThrValAspGlyProTyrThrGlnSerCys 819
Db 301 AAATTCTGGCGGCAACCGCGAGTGCAGCAGCTGTGGATGGCGGTGCACACAGAGGTGC 360
Qy 820 GluAspSerAspLeuAspCysPheValIleAspAsnAsnGlyPheIleLeuIleSerLys 839
Db 361 GAGGACAGTATCTGGACTGCTTCGTCTATCGACAAACGCGTTCATTCTGATCTCCAAG 420
Qy 840 ArgSerArgGluThrGlyArgPheLeuGlyGluValAspGlyAlaValLeuThrGlnLeu 859
Db 421 AGGTCCCGAGAGACGGGAAGATTTCTGGGGAGGTGGATGGTGTCTGTCTGACCCAGCTG 480
Qy 860 LeuSerMetGlyValPheSerGlnValThrMetTyrAspTyrGlnAlaMetCysLysPro 879
Db 481 CTGAGCATGGGGTGTTCAGCCAAAGTACTATGTATGACTATTCAGGCCATGTGCACCAAC 540
Qy 880 SerSerHisHisSerAlaAlaGlnProLeuValSerProIleSerAlaPheLeuThr 899
Db 541 TCAGTCAACCAACACAGTGCAGCCAGCCCTGTGTGACGCCAATTTCTGCTTCTTGACG 600
Qy 900 AlaThrArgTTPLeuLeuGlnLeuValLeuPheLeuLeuGluTTPSerValTTPGly 919
Db 601 CGCAGCAGGTGGTGTCTGCGAGGAGCTGGTCTTCTGCTGGAGTGGAGTGTCTGGGGC 660
Qy 920 SerTTPArgArgGlyAlaGluAlaLysSerValPheHisHisLysHisLys 939
Db 661 TCTGTGTACACAGAGGGGCGAGGCCAAAGTGTCTTCCATCACTCCCAACCAACACAG 720
Qy 940 LysGlnAspProLeuGlnProCysAspThrGluTyrProValPheValTyrGlnProAla 959
Db 721 AAGCAGACCCGCTGCAGCCCTGCGACACGAGGTACCCCGTTCGTGTACCAAGCGGCC 780
Qy 960 IleArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLysValPheValGln 979
Db 781 ATCCGGAGAGCCAAACGGAGTCTGTGGAGTGGCGGCCCTGCCAGAGGTATTTGGTGTGAG 840
Qy 980 GlnIleProAsnSerAsnLeuLeuValThrAspProThrCysAspCysSerIle 999
Db 841 CAGATTTCCCAACAGTAACCTTCTCTCTGCTGTGACAGACCCCACTGTGTGAGTGTGAGCATC 900
Qy 1000 PheProValLeuGlnGluAlaThrGluValLysTyrAsnAlaSerValLysCysAsp 1019
Db 901 TTCCACCAAGTGTGACGAGGGGACAGAGTCAAATATAATGCTCTGTCAAATGTGAC 960
Qy 1020 ArgMetArg 1022
Db 961 CGGATGCGC 969
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RESULT 9

US-09-397-550-13

; Sequence 13, Application US/09397550

; Patent No. 678952

; GENERAL INFORMATION:

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; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCES: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 912
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-397-550-13
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Alignment Scores:

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Pred. No.: 7,47e-173 Length: 912
Score: 1598.00 Matches: 302
Percent Similarity: 99.67% Conservative: 1
Best Local Similarity: 99.34% Mismatches: 1
Query Match: 27.91% Indels: 0
DB: 4 Gaps: 0
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US-09-833-222a-10 (1-1090) x US-09-397-550-13 (1-912)

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Qy 700 AlaGlyLeuLeuArgSerSerLeuPheValGlySerGluLysValSerAspArgLysPhe 719
Db 1 AGTGGCTCTCTGAGAACGAGCTGTTGCTGGCTCCGAGAGGTCTCCGACAGGAAGTTC 60
Qy 720 LeuThrProGluAspGluAlaSerValPheThrLeuAspArgPheProLeuTyrPyrArg 739
Db 61 CTGACACCTGAGGACGAGGCGAGCTGTTCAACCTCGGACCGCTTCCGCGTGTGGTACCGC 120
Qy 740 GluAlaSerGluHisProAlaGlySerPheValPheAsnLeuArgTTPAlaGluGlyPro 759
Db 121 CAGGCTCAGAGCATCTCTGTGCGAGCTTCTTCAACCTCGCTGGGCGGAGGACCA 180
Qy 760 GluSerAlaGlyGluProMetValThrAlaSerThrAlaValAlaValThrValAsp 779
Db 181 GAAAGTGGGCTGAACCCATGGTGTGACGCGCAAGCACAGCTGTGGCGGTGACCGTGGAC 240
Qy 780 LysArgThrAlaIleAlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArg 799
Db 241 AAGAGACAGCCATTCTGCGAGCGCGGCGCTCCAAATGAAGCTGGAATTTCTTCCAGCGC 300
Qy 800 LysPheTTPAlaAlaThrArgGlnCysSerThrValAspGlyProTyrThrGlnSerCys 819
Db 301 AAATTCTGGCGGCAACCGCGAGTGCAGCAGCTGTGGATGGCGGTGCACACAGAGGTGC 360
Qy 820 GluAspSerAspLeuAspCysPheValIleAspAsnAsnGlyPheIleLeuIleSerLys 839
Db 361 GAGGACAGTATCTGGACTGCTTCGTCTATCGACAAACGCGTTCATTCTGATCTCCAAG 420
Qy 840 ArgSerArgGluThrGlyArgPheLeuGlyGluValAspGlyAlaValLeuThrGlnLeu 859
Db 421 AGGTCCCGAGAGACGGGAAGATTTCTGGGGAGGTGGATGGTGTCTGTCTGACCCAGCTG 480
Qy 860 LeuSerMetGlyValPheSerGlnValThrMetTyrAspTyrGlnAlaMetCysLysPro 879
Db 481 CTGAGCATGGGGTGTTCAGCCAAAGTACTATGTATGACTATTCAGGCCATGTGCACCAAC 540
Qy 880 SerSerHisHisSerAlaAlaGlnProLeuValSerProIleSerAlaPheLeuThr 899
Db 541 TCAGTCAACCAACAGTGCAGCCAGCCCTGTGTGACGCCAATTTCTGCTTCTTGACG 600
Qy 900 AlaThrArgTTPLeuLeuGlnLeuValLeuPheLeuLeuGluTTPSerValTTPGly 919
Db 601 CGCAGCAGGTGGTGTCTGCGAGGAGCTGGTCTTCTGCTGGAGTGGAGTGTCTGGGGC 660
Qy 920 SerTTPArgArgGlyAlaGluAlaLysSerValPheHisHisLysHisLys 939
Db 661 TCTGTGTACACAGAGGGGCGAGGCCAAAGTGTCTTCCATCACTCCCAACCAACACAG 720
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QY 940 LysGlnAspProLeuGlnProCysAspThrGluTyrProValPheValTyrGlnProAla 959
Db 721 AAGCAGGACCGCTGCGAGCCCTCGGACACGAGTACCCCGTTCGTTGTCACGCGGCC 780
QY 960 IleArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLysValPheValValGln 979
Db 781 ATCCGGAGGCCAACGGATCGTGGAGTGGCGGCCCTGCCAGAAAGTATTGTGGTGCAG 840
QY 980 GlnIleProAsnSerAsnLeuLeuLeuValThrAspProThrCysAspCysSerIle 999
Db 841 CAGATTCACCAACAGTAACCTCCTCCTCGTGACACAGCCACCTGTGTGATCGAGCATC 900
QY 1000 PheProProVal 1003
Db 901 TTCCACCAAGTG 912

RESULT 10
US-09-470-443-5
; Sequence 5, Application US/09470443
; Patent No. 6441156
; GENERAL INFORMATION:
; APPLICANT: Lerman, Michael I.
; APPLICANT: Minna, John D.
; APPLICANT: Latif, Farida
; APPLICANT: Wei, Ming-Hui
; APPLICANT: Sekido, Yoshitaka
; APPLICANT: Gao, Boning
; APPLICANT: Duh, Fuh-Mei
; TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
; FILE REFERENCES: NIH-05043
; CURRENT APPLICATION NUMBER: US/09/470,443
; CURRENT FILING DATE: 1999-12-22
; EARLIER APPLICATION NUMBER: 60/114,359
; EARLIER FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 5279
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (185)..(3415)
US-09-470-443-5

Alignment Scores:
Pred. No.: 1.63e-124 Length: 5279
Score: 1188.50 Matches: 349
Percent Similarity: 47.61% Conservative: 208
Best Local Similarity: 29.83% Mismatches: 432
Query Match: 20.76% Indels: 181
DB: 3 Gaps: 44

US-09-833-222A-10 (1-1090) x US-09-470-443-5 (1-5279)
QY 10 ArgAspArgValLysLeuTAlaAspThrPheGlyAspLeuTyrAsnThrValThr 29
Db 176 CGGGGCGTGTGACGACGCTCGGCGCGCGCTCGGAGCAGGAGTGTGACGCGCGTGTGCGG 235
QY 30 LysTyrSerGlySerLeuLeuGlnLysLysTyrLysAspValGluSerSerLys 49
Db 236 ATTTTGGAGCGCTCCAGCAGCTCCGTGAGATTTCACAGACAAACCGGAACCTGTTTCGAG 295
QY 50 IleGluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMet 69
Db 296 GTACAGAGAATGAGCCTCAGAAGTTGGTGGAGAAGTGGCGAGGACATTGAGAGCCTT 355
QY 70 LeuArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeu 89
Db 356 CTGCAGGAGAGTGTGAGGCGCTGAGAGAGCTGGTGTGCTGCAGAGAACTTCCAGAAA 415
QY 90 AsnHisGluPheAsnGluSerLeuValPheAsp-----TyrTyrAsnSerValLeu 106
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Db 416 GCACACCGCTGGCAGACACATCAAGGAGGAGACATCGTGTACTATGACGCCAAGGCT 475
QY 107 IleAsnGluArgAspGlu---LysGlyAsnPheValGluLeuGlyAla----- 121
Db 476 GACGCTGAGCTGACGACCGCTGAGAGTGTGAGAAAGGGGTCTAAGGCAGCACC 535
QY 122 -----GluPheLeuLeuGluSerAsnAlaHisPheSerAsnLeuProValAsnThr 138
Db 536 CTAAAGGCTGGACTTCATCGAGGACCCCAAC-----TTCAAGAAC---AAGGTCAACTAT 586
QY 139 SerIleSerValGlnLeuProThrAsnValTyrAsnLysAspProAspIleLeuAsn 158
Db 587 TCATACGCGGCTGTACAGATCCCTACGACATCTACAAAGGCTCCACTGTCTCATCTCAAT 646
QY 159 GlyValTyrMetSerGluAlaLeuAsnAlaValPheValGluAsnPheGlnArgAspPro 178
Db 647 GAGCTCAACTGGACAGAGGCCCTGGAGAATGTGTTCAAGAAACCGCAGACAGACCCC 706
QY 179 ThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhePheArgIleTyrProGlyIle 198
Db 707 ACACCTCTGTGGCAGGTCTTCGGCAGCGCCACAGGAGTCACTCGCTACTACCCGGCCACC 766
QY 199 LysTrpThrProAspGluAsnGlyValIleThrPheAspCysArgAsnArgGlyTyrTyr 218
Db 767 CCGTGGCGAGCCCCCAAGAAG---ATCGACCTGTACGATGTCGAGGAGACCCCTGGTAT 823
QY 219 IleGlnAlaAlaThrSerProLysAspIleValIleLeuValAspValSerGlySerMet 238
Db 824 ATCCAGGGGGCCCTCGTCACCAAGACATGTCATCATCTGTGATGTGATGTCAGTGTG 883
QY 239 LysGlyLeuArgMetThrIleAlaLysHisThrIleThrThrIleLeuAspThrLeuGly 258
Db 884 ACGGCTCTGACCTGAAGCTGATGAGACATCTGCTCGAGATGCTGACACGCTGTCT 943
QY 259 GluAsnAspPheValAsnIleAlaTyrAsnAspTyrValHisTyrIleGluProCys 278
Db 944 GATGATGACTATGTGAATGTGGCTCGTTCACGAGAGGACAGCCTGTGTCA---TGC 1000
QY 279 PheLysGlyIleLeuValGlnAlaAspArgAspAsnArgGluHisPheLysLeuVal 298
Db 1001 TTCACACAC---CTGGTGCAGGCCCAATGTGCGCAACAAGAAGGTGTTCAGGAAGTGTG 1057
QY 299 GluGluLeuMetValLysGlyValGlyValValAspGlnAlaLeuArgGluAlaPheGln 318
Db 1058 CAGGGCATGTGGCCCAAGGCGCACAGGCTACAGGCGGCTTTCAGTATGCTTGTGAC 1117
QY 319 IleLeuLysGlnPheGlnGluAlaLysGlnGlySerLeuCysAsnGlnAlaIleMetLeu 338
Db 1118 CAGCTGCAGAACTCCAAACATCACTCGGGCCAAC-----TGCAACAAGATGATCATGATG 1171
QY 339 IleSerAspGlyAlaValGluAspTyrGluProValPheGluLysTyrAsnTyrProAsp 358
Db 1172 TTCACGGATGGTGGTGGAGGACCGCTGCGAGGACGCTCTTTTGAGAAGTACAAATTTGCCCAAC 1231
QY 359 CysLysValArgValPheThrTyrLeuIleGlyArgGluValSerPheAlaAspArgMet 378
Db 1232 CGGACGGTGGCGGTGTTTACTTCTCCGTGGGCGCAGCATAACTATGACGTACACCGCTG 1291
QY 379 LysTrpIleAlaCysAsnAsnLysGlyTyrTyrThrGlnIleSerThrLeuAlaAspThr 398
Db 1292 CAGTGGATGGCTGTGCCAACAAAGGCTACTATTTTGAGATCCCTTCCATCGGAGCATC 1351
QY 399 GlnGluAsnValMetGluTyrLeuHisValLeuSerArgProMetValIle-----Asn 416
Db 1352 CGCATCAACACACAGGAATATCTAGATGTGTGGGCGAGGCCCATGTGTGCTGGCAGCAAG 1411
QY 417 HisAspHisAspIleIleTrpThrGluAlaTyrMetAspSerLysLeuLeuSerSerGln 436
Db 1412 GAGGCCAAGCAGGTTTCAGTGGACCAACGCTGTATGAGAT----- 1450
QY 437 AlaGlnSerLeuThrLeuLeuThrThrValAlaMetProValPheSer----- 452
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Db 1451 GCACTGGGACTGGGGTTGGTGAACAGGGACCTCCCTGTTTCAACCTGCACACAGGAT 1510
Qy 453 -----LysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGly 468
Db 1511 GGCCCTGGGAAAGAAACCAG-----CTGATCCTGGGGTGTATGGC 1555
Qy 469 SerAspValAlaLeuArgGluMetLysLeuAlaProArgTyrLysLeuGlyValHis 488
Db 1556 ATTGACGTGCTCTGAATGACATCAAGAGGTGACCCCACTACACGCTGGAGCCAAC 1615
Qy 489 GlyTyrAlaPheLeuAnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgPro 508
Db 1616 GGCTATGTTGGCATTTGACCTGGAACGGGTACGTGTGTGTCACCCCAATCTCAAGCCC 1675
Qy 509 Leu-----TyrArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerVal 525
Db 1676 CAGACCACCAACTTCCGGGAGCCTGTGACTCG----- 1708
Qy 526 AspLeuSerGluValGluTrpGluAspGln---AlaGluSerLeuArgThrAlaMetIle 544
Db 1709 GACTTCTGATCGGAGCTAGAGATGAGAAAGAGAGATCCGTCGGAGCATGATT 1768
Qy 545 AsnArgGluThrGlyThrLeuSerMetAspValLysValProMetAspLysGlyLysArg 564
Db 1769 GATGGCAACAGGGCCCAACAGCAGATCAGAACGTTGTGTCAGTCCCTGGATGAGAGTAC 1828
Qy 565 ValLeuPheLeuThrAsnAspTyrPhePheThrAspIleSerAspThrProPheSerLeu 584
Db 1829 ATAGATGAGGTGACACCGAAGTACACCTGGGTGCTATAGGAGCATTACTACAGGCTG 1888
Qy 585 GlyAlaValLeuSerArgGlyHisGlyGluTyrIle----- 596
Db 1889 GGGCTGTGTCCCAACCTACAGCACCTTCTACCTCCAAGCCAACTCTCAGTGACCAGATC 1948
Qy 597 -----LeuLeuGlyAsnThrSerValGluGluGlyLeuHis 608
Db 1949 CTCGAGTCAAGTATTTGAGTTCCTGCTCCCGAGCTTTGAGTCTGAAGGA---CAC 2005
Qy 609 AspLeuLeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIle 628
Db 2006 GTTTTCATTGCTCCACA-----GAGTACTGC---AAGGACTGT 2041
Qy 629 AspProAspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLys 648
Db 2042 AATGCCCTCAGACAACAACCGAGTTCCTGAAAACTTTATTGAGCTCATGGAGAAAGTG 2101
Qy 649 AspProAsp---LeuGluCysAspGluLeuValArgGluValLeuPheAspAlaVal 667
Db 2102 ACTCCAGACTCCAAGCAGTGCACAACCTTCTCTGCACAACTGATCTTGGACACCGGC 2161
Qy 668 ValThrAlaProMet---GluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGlu 686
Db 2162 ATCAGCAGCAGCTGTGTAGAGCTGTGTGGAGGACCAGGATCTCAAC----- 2209
Qy 687 SerGluHisValValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSer 706
Db 2210 ---ACGTACAGCTTACTGGCGCTGTCGTCACACAGCGTGGCATCACCGCA----- 2260
Qy 707 LeuPheValGlySerGluLysValSerAspArgLysPheLeuThrProGluAspGluAla 726
Db 2261 -----GTCCTCCCAACAAGGCAGCT 2281
Qy 727 SerValPheThrLeuAspArgPheProLeu-----TrpTyrArgGlnAlaSerGlu 743
Db 2282 GAGGACTGGACAGAGAACCCCTGAGCCCTTCAATGCCAGCTTCTACCGCCGAGCTTGAT 2341
Qy 744 HisProAlaGlySerPheValPheAsn-----LeuArgTrpAla 756
Db 2342 AAC-----CACGTTTATGTCTTCAAGCCCCCAACACGAGGATGCCCTGTTAAGG----- 2389
Qy 757 GluGlyPro---GluSerAlaGlyGluProMetValThrAlaSerThrAlaValAla 775
Db 2390 -----CCGTGGAGCTGGAGATGACACTGTGGGCATCTCTGTCAGACAGCTGTGGAG 2443

Qy 776 ValThrValAspLysArgThrAlaIleAlaAlaAlaGlyValGlnMetLysLeuGlu 795
Db 2444 CTCAGCTAGGCGGCGCACACTGAGCGCAGCAGTGGTGGCGTCAAGCTGGACCTAGAG 2503
Qy 796 PheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThrValAspGlyProTyr 815
Db 2504 GCTTGGGCTGAGAAGTTTCAAGGTGTAGCCAGCAACGTATCCCAACCAAGCACCT--- 2560
Qy 816 ThrGlnSerCys-----GluAspSerAsp 823
Db 2561 ---CAGAGTTCGGGCCCAACAGCCACTGTGAGATGAGCTGCCGAGGTTTAACAATGAGGAC 2617
Qy 824 LeuAspCysPheValIleAspAsnAsnGlyPheIleLeuIleSerLysArgSerArg--- 842
Db 2618 TTACTCTGTCTCATTTGATGAGGAGTTCCTGTGTCTGTCATCAACCAAGCAACATCAG 2677
Qy 843 -----GluThrGlyArgPheLeuGlyGluValAspGlyAlaValLeuThrGlnLeu 860
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Qy 861 SerMetGlyValPheSerGlnValThrMetTyrAspTyrGlnAlaMetCysLysProSer 880
Db 2738 AATAACTCTTCTACACCCCAAGGAGTCTCTATGACTATCAGGAGGCTGTGCCCTCAG 2797
Qy 881 SerHisHisSerAlaAlaGlnPro-----LeuValSerProIleSerAlaPhe 897
Db 2798 CCCCTGGCAACCTGGGTGCTGCACCCCGGGTGTCTTTGTGCCACCGTGTGCAGATTTC 2857
Qy 898 Leu-----ThrAlaThrArgTrpLeuLeuGlnGluValLeuPhe 911
Db 2858 CTTAACTGCGCTGTGGAGCTCTGTGCGCCCTGGTCCCTGTTCCAGAGCTTCTCTAC 2917
Qy 912 LeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGly-----AlaGluAla 928
Db 2918 GGCTC-----ATCTACCACAGCTGTGTTCCAAACAGACACCCCGCGGAGCGGAGGG 2968
Qy 929 LysSerValPheHisHisSerHisLysHisLysGlnAspProLeuGlnProCysAsp 948
Db 2969 AGCCCGAGAGCGCGAGAGCAGCTGCGTCATGAACAG----- 3007
Qy 949 ThrGluTyrProValPheValTyrGlnProAlaIleArgGluAla---AenGlyIleVal 967
Db 3008 ACCGATPAC-----TACTCGCTCGGTAAACCGCTCTCTACAGCCCATCATC 3055
Qy 968 GluCysGlyProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeu 987
Db 3056 GACTGGGAAACTGCTCCAGGCTGTTCCACGCGCAGAGACTGACCAACACCAATCTTCTC 3115
Qy 988 LeuLeuValThrAsp---ProThrCysAspCysSerIlePheProProValLeuGlnGlu 1006
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Qy 1007 AlaThrGluValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeu 1026
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Db 3236 CGGAGAGCGCGGCATCTGCTTCGACTACAAACGCGACAGAGATACCTCAGACTGTGGC 3295
Qy 1046 ArgGlyTrpAlaGlyPhe-----SerSerProAsnProLeu 1057
Db 3296 CGCGGG---GCCCTCTTCCCGCGCTCGCTGGGGGTCTGCTGCTCTCCCTGCACTGCTGCTC 3352
Qy 1058 CysLeuGlyLeuCysProCysArgGlnGluHisIleGlyMet----- 1071
Db 3353 CTCTGGGCTGCGCGCGCGCGCGCAGCTCTCAAGTCTCTCCAGCGCTCTCGCGCGCTC 3412
Qy 1072 -----ProMetAsnThrProValProVal 1079
Db 3413 TGAGCACCTGCCCGCCACCCCTCCACTC 3442

RESULT 11

US-09-470-443-1
: Sequence 1, Application US/09470443
: Patent No. 6441156
: GENERAL INFORMATION:
: APPLICANT: Lerman, Michael I.
: APPLICANT: Minna, John D.
: APPLICANT: Latif, Farida
: APPLICANT: Wei, Ming-Hui
: APPLICANT: Sekido, Yoshitaka
: APPLICANT: Gao, Boning
: APPLICANT: Duh, Fuh-Wei
: TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
: FILE REFERENCE: NIH-05043
: CURRENT APPLICATION NUMBER: US/09/470,443
: CURRENT FILING DATE: 1999-12-22
: EARLIER APPLICATION NUMBER: 60/114,359
: EARLIER FILING DATE: 1998-12-30
: NUMBER OF SEQ ID NOS: 114
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 5463
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (162)..(3599)
US-09-470-443-1

Alignment Scores:

Pred. No.: 2,26e-124 Length: 5463
Score: 1187.50 Matches: 348
Percent Similarity: 47.59% Conservatives: 206
Best Local Similarity: 29.90% Mismatches: 429
Query Match: 20.74% Indels: 181
DB: 3 Gaps: 44

US-09-833-222A-10 (1-1090) x US-09-470-443-1 (1-5463)

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QY 36 LeuLeuGlnLysTyrLysAspValGluSerSerLeuLysIleGluGluValAspGly 55
DB 438 CAGCTCGTCGAGATTTACAGGACACCGGAACCTGTTCCAGGTACAGGAGATGAGCCT 497
QY 56 LeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArgLysValGlu 75
DB 498 CAGAAGTTGGTGAGAGAGGTGGCAGGGGACATTGAGAGCCCTTCTGGACAGGAAGGTGCAG 557
QY 76 AlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsnHisGluPheAsnGlu 95
DB 558 GCCTGNAGAGACTGGCTGATGTGCAGAGAACTTCAGAAACACACCGCTGGCAGGAC 617
QY 96 SerLeuValPheAsp-----TyrTyrAsnSerValLeuIleAsnGluArgAspGlu 112
DB 618 AACATCAAGGAGGACAGACATCGTGTACTATGACGCCAAGCTCAGCGCTGAGCTGGAGCAG 677
QY 113 ---LysGlyAsnPheValGluLeuGlyAla-----GluPheLeu 124
DB 678 CCTGAGAGTAGGATGTGGAAAGGGGGTCTAAGGCCAGCACCCCTAAGGCTGGACTTCATC 737
QY 125 LeuGluSerAsnAlaHisPheSerAsnLeuProValAsnThrSerIleSerSerValGln 144
DB 738 GAGGACCCAAAC-----TTCAAGAAC--AAGGTCAACTATTTCATACGGCGGTGTACAG 788
QY 145 LeuProThrAsnValTyrAsnLysAspProAspIleLeuAsnGlyValTyrMetSerGlu 164
DB 789 ATCCCTACGGACACTACAAAGGCTCCACTGTCTCATCTCAATGAGCTCAACTGACAGAG 848
QY 165 AlaLeuAsnAlaValPheValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyr 184

DB 849 GCCCTGGAGAATGTGTTTCATGGAAACCGCAGACAAGACCCACACTGCTGTGGCAGGTC 908
QY 185 PheGlySerAlaThrGlyPhePheArgIleTyrProGlyIleLysTyrThrProAspGlu 204
DB 909 TTCGGCAGCGCCACAGGAGTCACTCGCTACTACCCGGCCACCCGCTGGCGAGCCCCCAAG 968
QY 205 AsnGlyValIleThrPheAspCysArgAsnArgGlyTyrTyrIleGlnAlaAlaThrSer 224
DB 969 AAG--ATCGACCTGTACGATGTCGGAAGGAGACCTGGTATATCCAGGGGGCCTCGTCA 1025
QY 225 ProLysAspIleValIleLeuValAspValSerGlySerMetLysGlyLeuArgMetThr 244
DB 1026 CCAAAAGACATGTCATCTGTCGATGTGAGTGGCAGTGTGAGCGCCCTGACCCCTGAAG 1085
QY 245 IleAlaLysHisThrIleThrIleLeuAspThrLeuGlyGluAsnAspPheValAsn 264
DB 1086 CTGATGAAGACATCTGTCTGCGAGATGTCGACCGCTGCTGATGATGACTATGTGAAT 1145
QY 265 IleAlaLysAsnAspTyrValHisTyrIleGluProCysPheLysGlyIleLeuVal 284
DB 1146 GTGGCCTCGTTCAACGAGAAGGCACAGCCTGTGTCA--TGCCTTCACACAC--CTGGTG 1199
QY 285 GlnAlaAspArgAsnArgGluHisPheLysLeuValGluGluLeuMetValLys 304
DB 1200 CAGGCCAATGTGCGCAACAAGAGGTGTTTCAAGGAAGCTGTGCGGGCATGGTGGCCAAAG 1259
QY 305 GlyValGlyValValAspGlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGln 324
DB 1260 GGCACACACAGGCTACAGGGCGGCTTGTAGTATGCTTTGACCAGCTGCAGAACTCCAAC 1319
QY 325 GluAlaLysGlnGlySerLeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaVal 344
DB 1320 ATCACTCGGCGCCAAAC--TGCAACAAGATCATCATGATGTTACGGATGGTGGTGAG 1373
QY 345 GluAspTyrGluProValPheGluLysTyrAsnTyrProAspCysLysValArgValPhe 364
DB 1374 GACCGCGTCGACGAGCGTCTTTGAGAAGTACAATTGGCCAAACCGGACGGTGGCGTGT 1433
QY 365 ThrTyrLeuIleGlyArgGluValSerPheAlaAspArgMetLysTrpIleAlaCysAsn 384
DB 1434 ACTTTCCTCGTGGGCGCATTAATACTATGAGTCACACCGCTGCGATGGATGGCTGTGCC 1493
QY 385 AsnLysGlyTyrTyrThrGlnIleSerThrLeuAlaAspThrGlnGlnAsnValMetGlu 404
DB 1494 AACAAAGGCTACTATTTTTCAGATCCCTTCATCGGAGCCATCCGATCAACACACAGGAA 1553
QY 405 TyrLeuHisValLeuSerArgProMetValIle-----AsnHisAspHisAspIleIle 422
DB 1554 TATCTAGATGTGTGGCGAGGCCCATGTTGCTGGCAGGCAAGGAGGCCAAGCAGGTTTCAG 1613
QY 423 TrpThrGluAlaTyrMetAspSerLysLeuLeuSerSerGlnAlaGlnSerLeuThrLeu 442
DB 1614 TGGACCAACGTGTATGAGGAT-----GCACTGGGACTGGGGTTG 1652
QY 443 LeuThrThrValAlaMetProValPheSer-----LysLys 454
DB 1653 GTGGTAAACAGGAGCCCTCCCTGTTTTCACACTGACACAGATGGCCCTGGGGAAGAAAG 1712
QY 455 AsnGluThrArgSerHisGlyIleLeuLeuGlyValValIcLysSerAspValAlaLeuArg 474
DB 1713 AACCAAG-----CTGATCTGGGCGTGTATGGGCATTGACGGCTCTGAAT 1757
QY 475 GluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyrAlaPheLeuAsn 494
DB 1758 GACATCAAGAGGCTGACCCCAACTACACGCTTGGAGCCACCGCTATGTGTTTGGCATT 1817
QY 495 ThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeu-----TyrArg 511
DB 1818 GACCTGAACGGGTACGTGTTGTCTGCACCCCAATCTCAAGCCCGACACCACTTCCGG 1877
QY 512 GluGlyLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluValGlu 531
DB 1878 GAGCCTGTGACTCTG-----GACTTCTGGATGGGAG 1910

Qy	532	TrpGluAspGln----	AlaGluSerLeuArgThrAlaMetIleAenArgGluThrGlyThr	550
Db	1911	CTAGAGATGAGAA	CAAGGAAGATCCGTGGGAGCATGATTGATGTGCAACAAGGGCCAC	1970
Qy	551	LeuSerMetAspVal	LeuValProMetAspLysGlyLysArgValLeuPheLeuAsn	570
Db	1971	AAGCAGATCAGAA	CGTTGGTCAAGTCCCTGGATGAGAGGTACATAGATGAGGTGACACGG	2030
Qy	571	AspTyrPhePheThrAsp	IleSerAspThrProPheSerLeuGlyAlaValLeuSerArg	590
Db	2031	AACACACCTCGGT	GGTCCCTATTAAGGAGCACTAACTACACCGCTGGGCGTGGTCTCCCAACC	2090
Qy	591	GlyHisGlyGluTyrIle-	-----	596
Db	2091	TACAGCACCTTCT	ACCTCCCAAGCCAACTCTCAGTGACCAGATCTCTGCAGGTCAAGTATTTT	2150
Qy	597	-----	LeuLeuGlyAenThrSerValGluGluGlyLeuHisAspLeuLeuHisProAsp	614
Db	2151	GAGTTCTCTGCC	CAGCAGCTTTGAGTCTGAAGCA--CACGTTTTTCATTGTCTCCCGAGA	2207
Qy	615	LeuAlaLeuAlaGlyAsp	TpIleTyrCysIleThrAspIleAspProAspHisArgLys	634
Db	2208	-----	-----GAGTACTGC--AAGCACTCGAATGCTCTCAGACAACAAC	2243
Qy	635	LeuSerGlnLeuGluAla	MetIleArgPheLeuThrArgLysAspProAsp--LeuGlu	653
Db	2244	ACCGAGTTCTG	AAAACTTTATTGAGCTCATGGAGAAAGTGACTCCAGACTCCAGCAG	2303
Qy	654	CysAspGluGluLeu	ValArgGluValLeuPheAspAlaValValThrAlaProMet---	672
Db	2304	TGCAACAACCTCT	CTCTGCAACACTGATCTTGACACGGCGCATCACGACGAGCTGGTA	2363
Qy	673	GluAlaTyrTrpThrAla	LeuAlaLeuAsnMetSerGluGluSerGluHisValValAsp	692
Db	2364	GAGCGTGTGG	AGGACCGAGTCTCAAC-----ACGTACAGCTACTGT	2408
Qy	693	MetAlaPheLeuGlyThr	ArgAlaGlyLeuLeuArgSerSerLeuPheValGlySerGlu	712
Db	2409	GCGGTGTTGCT	GCACACAGCGGTGGCATCACCCGA-----	2444
Qy	713	LysValSerAspArgLys	PheLeuThrProGluAspGluAlaSerValPheThrLeuAsp	732
Db	2445	-----	GTCTCCCAACAAGGCAGCTGAGGACTCGACAGAGAAC	2483
Qy	733	ArgPheProLeu-----	TrpTyrArgGlnAlaSerGluHisProAlaGlySerPhe	749
Db	2484	CCTGAGCCCTTCA	ATGCGAGCTTCTACCGCGCAGCTGGATAAC-----CACGGTTAT	2537
Qy	750	ValPheAsn-----	-----LeuArgTrpAlaGluGlyPro-----GluSer	761
Db	2538	GTCTTCAAGGCC	CCCCACACAGGATGCCCTGTTAAG-----CCGCTGGAGCTG	2585
Qy	762	AlaGlyGluProMetVal	ValThrAlaSerThrAlaValAlaValThrValAspLysArg	781
Db	2586	GAGATGACACTGT	GGGCATCTCTCGTCAGCACAGCTGTGAGCTCAGCTTAGCGAGCGCC	2645
Qy	782	ThrAlaIleAlaAla	AlaGlyValGlnMethLysLeuGluPheLeuGlnArgLysPhe	801
Db	2646	ACACTGAGCCAG	CAGTGGTGGCGCTCAAGCTGGACCTAGAGGCTTGGGCTGGAGAGTTTC	2705
Qy	802	TrpAlaAlaThrArgGln	CysSerThrValAspGlyProTyrThrGlnSerCys-----	819
Db	2706	AAGGTGTGCC	AGCAACCGTACCCACCAAGACGAGCCT-----CAGAAGTCGGGCCCC	2759
Qy	820	-----	-----GluAspSerAspLeuAspCysPheValIle	829
Db	2760	AACAGCCACTGT	GAGTGGACTCGAGGTTAAACAATGAGGACTTACTCTGTGTCTCTATT	2819
Qy	830	AspAsnAsnGlyPhe	IleLeuIleSerLysArgSerArg-----GluThrGlyArg	846
Db	2820	GATGATGGAGGAT	TCTCGTGTCAACACCAAGCATCAGTGGGACCAAGTGGGCAGG	2879

Qy	847	PheLeuGlyGluValAlaAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSer	866
Db	2880	TTCTTCAGTGGAGTGATGCAACCTGATGCTGGCACTCTACAAATACTCTTCTTCAACCC	2939
Qy	867	GlnValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisHisSerAla	886
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Db	2940	CGCAAGGAGTCTATGACTATATCAGGCAGCCTGTGCCCTCAGCCCTCGCAACCTGGGT	2999
Qy	887	AlaGlnPro-----LeuValSerProIleSerAlaPheLeu-----	898
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Qy	899	---ThrAlaThrArgTrpLeuLeuGlnGluValLeuPheLeuLeuGluTrpSerVal	917
Db	3060	ACTCTGCTGCCCGCTGGTCCCTGTTCCAGCAGCTTCTCTACGGCCTC-----ATC	3110
Qy	918	TrpGlySerTrpTyrAspArgGly-----AlaGluAlaLysSerValPheHisHis	934
Db	3111	TACCACAGCTGGTTTCCAAGCAGACCCCGCGGAGCGCGAGGGAGCCCGAGACGCGCGAG	3170
Qy	935	SerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrProValPhe	954
Db	3171	AGCAGCTGCGTCTATGAACAG-----ACCCAGTAC-----	3200
Qy	955	ValTyrGlnProAlaIleArgGluAla---AsnGlyIleValGluCysGlyProCysGln	973
Db	3201	---TACTTCGGCTCGGTAAAGCGCTCTCTACACGCCATCATCGACTCGCGAACTGCTCC	3257
Qy	974	LysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuValThrAsp---	992
Db	3258	AGGCTGTTCCACGCGCAGAGACTGACCAACACCAATCTTCTCTTTGGTGGCGCAGAA	3317
Qy	993	ProThrCysAspCysSerIlePheProProValLeuGlnGluAlaThrGluValLysTyr	1012
Db	3318	CCGCTGTGCAGCCAGTGCAGGCTGCGCGCTCTCGAAGAAGAGACGCACTGCCCAGCG	3377
Qy	1013	AsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArgProAspSer	1032
Db	3378	GACGGCCCGGAGCAGTGTGAGCTAGTGCAGAGACCCGGATACCGAGAGCGCCGCACATC	3437
Qy	1033	CysHisAlaPheHis---ProGluValAlaArgValGluAlaAspArgGlyTrpAlaGlyPhe	1051
Db	3438	TGCTTCGACTACAAACGACGACAGAAAGATACCTCAGACTGTGGCCGCGGG---GCCTCCTTC	3494
Qy	1052	-----SerSerProAsnProLeuCysLeuGlyLeuCysPro	1063
Db	3495	CCGCCGTGCTGGGGGTCTGTGTCCTCCCTGCAACTGCTCTCTCTGCGCCTTGC	3554
Qy	1064	CysArgGlnGluHisIleGlyMet-----ProMetAsnThr	1075
Db	3555	CGGCCGAGCCTCAAGTCTCTCGTCCACGCGCTCTGCGCGCCTCTGAGCACCTTGC	3614
Qy	1076	ProValProVal	1079
Db	3615	CCACCTCCACTC	3626

RESULT 12
US-09-470-443-3
; Sequence 3, Application US/09470443
; Patent No. 6441156
; GENERAL INFORMATION:
; APPLICANT: Lerman, Michael I.
; APPLICANT: Minna, John D.
; APPLICANT: Latif, Farida
; APPLICANT: Wei, Ming-Hui
; APPLICANT: Sekido, Yoshitaka
; APPLICANT: Gao, Boning
; APPLICANT: Duh, Fuh-Mei
; TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
; FILE REFERENCE: NIH-05043
; CURRENT APPLICATION NUMBER: US/09/470,443
; CURRENT FILING DATE: 1999-12-22
; EARLIER APPLICATION NUMBER: 60/114,359

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; EARLIER FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 5482
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; ORIGIN:
; NAME/KEY: CDS
; LOCATION: (181)..(3618)
US-09-470-443-3

Alignment Scores:
Pred. No.: 2,28e-124 Length: 5482
Score: 1187.50 Matches: 348
Percent Similarity: 47.59% Conservative: 206
Best Local Similarity: 29.90% Mismatches: 429
Query Match: 20.74% Indels: 181
DB: 3 Gaps: 44

US-09-833-222A-10 (1-1090) x US-09-470-443-3 (1-5482)

QY 16 TrpAlaAspThrPheGlyAspLeuTyrAsnThrValThrLysTyrSerGlySerLeu 35
Db 397 TGGGCGCGCGCTCGGAGCAGGAGGTCGACGGCGTGATCGCGATTTTGGAGGCGTCCAG 456
QY 36 LeuLeuGlnLysTyrLysAspValGluSerSerLeuLysIleGluGluValAspGly 55
Db 457 CAGCTCCGTGAGATTACAGGACAAACCGGAACCTGTTGAGGTACAGGAGATGAGCCT 516
QY 56 LeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArgLysValGlu 75
Db 517 CAGAAGTGTGTGAGAAAGTGGCAGGAGCATTTGAGAGCTTCTGGACAGGAGGTGCAG 576
QY 76 AlaValGlnAsnLeuValGluAlaGluGluAlaAspLeuAsnHisGluPheAsnGlu 95
Db 577 GCCTTGAAGAGACTGTGCTGTCAGAGAACTTCCAGAAACACACACCGCTGGCAGGAC 636
QY 96 SerLeuValPheAsp-----TyrTyrAsnSerValLeuIleAsnGluArgAspGlu 112
Db 637 ACATCAAGGAGGAGACATCTGTGTACTATGACGCCAAGGCTGACGCTGAGCTGGAGCAG 696
QY 113 ---LysGlyAsnPheValGluLeuGlyAla-----GluPheLeu 124
Db 697 CCTGAGAGTGAGGATGTGAAAGGGGGTCTAAGGCCAGCACCTAAGGCTGGACTTCATC 756
QY 125 LeuGluSerAsnAlaHisPheSerAsnLeuProValAsnThrSerIleSerSerValGln 144
Db 757 GAGGACCCCAAC-----TTCAAGAAC---AAGGTCAACTATTTCATACGCGGTGTACAG 807
QY 145 LeuProThrAsnValTyrAsnLysAspProAspIleLeuAsnGlyValTyrMetSerGlu 164
Db 808 ATCCCTACGGACATCTACAAAGGCTCCACTGTCTATCTCAATGAGCTCAACTGGACAGAG 867
QY 165 AlaLeuAsnAlaValPheValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyr 184
Db 868 GCCCTGGAGAAATGTGTTCTGAAACACCGCAGACAGACCCACACTGCTGTGGCAGGTC 927
QY 185 PheGlySerAlaThrGlyPhePheArgIleTyrProGlyIleLysTrpThrProAspGlu 204
Db 928 TTCGGAGCGGCCACAGAGGTCACTCTACTACCGGCCACCCCGCGGAGCGCCCAAG 987
QY 205 AsnGlyValIleThrPheAspCysArgAsnArgGlyTyrTyrIleGlnAlaThrSer 224
Db 988 AAG---ATGACCTGTACGATGTCCGAAGGAGACCTGTGTATATCCAGGGGCGCTCGTCA 1044
QY 225 ProLysAspIleValIleLeuValAspValSerGlySerMetLysGlyLeuArgMetThr 244
Db 1045 CCCAAAGACATGCTCATCTCGTGGATGTGAGTGGCAGTGTGAGCGCCTGACCCCTGAAG 1104
QY 245 IleAlaLysHisThrIleThrIleLeuAspThrLeuGlyGluAsnAspPheValAsn 264
Db 1105 CTGATGAAGACATCTGTCTGCGAGATGCTGGACACGCTGCTGTGATGATGATGTGAAT 1164

; 265 IleIleAlaTyrAsnAspTyrValHisTyrIleGluProCysPheLysGlyIleLeuVal 284
; 1165 GTGGCCTCGTTCAACAGGAAGGCACAGCCTGTGTCA---TGCTTCACACAC---CTGGTG 1218
; 285 GlnAlaAspArgAspAsnArgGluHisPheLeuValGluLeuValGluLeuMetValLys 304
; 1219 CAGGCCAATGTGCGCAACAAGAAGGTGTTCAAGGAAGCTGTGCAGGGCATGGTGGCCAAG 1278
; 305 GlyValGlyValValAspGlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGln 324
; 1279 GGCACCACAGGCTACAAAGCGCGCTTTGAGTATGCTTTGACCAGCTGCAGAACTCCAAC 1338
; 325 GluAlaLysGlnGlySerLeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaVal 344
; 1339 ATCACTCGGGCCCAAC-----TGCAACAAGATGATCATGATTTACAGATGTGTGTGAG 1392
; 345 GluAspTyrGluProValPheGluLysTyrAsnTrpProAspCysLysValArgValPhe 364
; 1393 GACCGCGTGCAGGACGCTCTTTGAGAAGTACAATTGSCCAACCGGACGGTGCCTGTTT 1452
; 365 ThrTyrLeuIleGlyArgGluValSerPheAlaAspArgMetLysTrpIleAlaCysAsn 384
; 1453 ACTTTCTCGGTGGGCGAGCATAACTATGACGTCACACCGCTGCAGTGGATGGCTGTGCC 1512
; 385 AsnLysGlyTyrTyrThrGlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGlu 404
; 1513 AACAAAGGTACTATTTTGAGATCCCTTCATCGGAGCCATCCGCATCAACACACAGGAA 1572
; 405 TyrLeuHisValLeuSerArgProMetValIle-----AsnHisAspIleIle 422
; 1573 TATCTAGATGTGTGGGAGGCCATCTGTGCTGGCAGCAAGGAGGAGCAAGAGTTTCAAG 1632
; 423 TrpThrGluAlaTyrMetAspSerLysLeuLeuSerSerGlnAlaGlnSerLeuThrLeu 442
; 1633 TGGACCAACGCTGTATGAGGAT-----GCATGGGACTGGGGTGTG 1671
; 443 LeuThrThrValAlaMetProValPheSer-----LysLys 454
; 1672 GTGGTAAAGGAGGACCTCTCTGTTTCAACCTGACACAGAGTGGCCTGGGGAAGAAGAG 1731
; 455 AsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAspValAlaLeuArg 474
; 1732 AACCAAG-----CTGATCTCTGGCGCTGATGGCATTGACGTGGCTCTGAAT 1776
; 475 GluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyrAlaPheLeuAsn 494
; 1777 GACATCAAGAGGCTGACCCCAACTACACGCTTGGAGCCACGCGCTATGTGTTTGCATT 1836
; 495 ThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeu-----TyrArg 511
; 1837 GACCTGACGGCTACGTGTGTGTCACCCCACTCAAGCCCGCAGACCCCACTTCCGG 1896
; 512 GluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluValGlu 531
; 1897 GACGCTGTGACTCTG-----GACTTCTGGATGGGAG 1929
; 532 TrpGluAspGln---AlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
; 1930 CTAGAGGATGAGAACAAAGAGAGATCCGTCGGAGCATGATTGATGGCAACAGGGCCAC 1989
; 551 LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570
; 1990 AAGCAGATCAGAACGTTGTTGTCAGTCCCTGGATGAGAGGTACATAGATGAGGTGACACGG 2049
; 571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
; 2050 AACTACACCTGGGTGCTATTAAGGAGCACTAACTACAGCCTGGGGCTGTGCTCCACCC 2109
; 591 GlyHisGlyGluTyrIle----- 596
; 2110 TACAGCACCTTCTACTCTCAAGCCCAATCTCAGTGACCAGATCCTGCGAGGTCAAGTATTTT 2169
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QY 597 -----LeuLeuGlyAenThrSerValGluGluGlyLeuHisAspLeuLeuHisProAsp 614
D 1710 GAGTTCCTGCTCCAGCAGCAGCTTTGAGTCTGAAGGA---CACGTTTTCATTGCTCCAGGA 2226
QY 615 LeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspProAspHisArgLys 634
D 2227 -----GAGTACTGC---AAGGACCTGGAATGCTCAGACAACAAC 2262
QY 635 LeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspProAsp---LeuGlu 653
D 2263 ACCGAGTCTCGAATAAACTTTATTGAGCTCATGGAGAAAGTACTCCAGACTCCAGCAG 2322
QY 654 CysAspGluLeuValArgGluValLeuPheAspAlaValValThrAlaProMet--- 672
D 2323 TGCACAACAACTTCTTCTGCAACAACCTGATCTGACACGGGCATCAGCGAGCTGGTA 2382
QY 673 GluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisValValAsp 692
D 2383 GAGCGTGTGGAGGGACCAAGGATCTCAAC-----ACGTACAGCCTACTG 2427
QY 693 MetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGlySerGlu 712
D 2428 GCCGTGTCTGCCACAGACGGTGGCATCACCGA----- 2463
QY 713 LysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeuAsp 732
D 2464 -----GTCTTCCCAACAAGGACGCTGAGGACTGGACAGAGAAC 2502
QY 733 ArgPheProLeu-----TrpTyrArgGlnAlaSerGluHisProAlaGlySerPhe 749
D 2503 CTGAGGCCCTTCAATGCCAGCTTCTACCGCGGAGCTGGATTAAC-----CACGGTTAT 2556
QY 750 ValPheAsn-----LeuArgTrpAlaGluGlyPro---GluSer 761
D 2557 GTCTTCAAGCCCCCAACACAGGATGCCCTGTAAAG-----CCGCTGGAGCTG 2604
QY 762 AlaGlyGluProMetValValThrAlaSerThrAlaValAlaValThrValAspLysArg 781
D 2605 GAGATGACACTGTGGCATCTCTCGTCAGCACAGCTGTGGAGCTCAGCCTAGGACGGCGC 2664
QY 782 ThrAlaIleAlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPhe 801
D 2665 ACACCTGAGGCCAGCAGTGGTGGCGCTCAAGCTGAGCCTAGAGCTTGGGCTGAGAAGTTC 2724
QY 802 TrpAlaAlaThrArgGlnCysSerThrValAspGlyProTyrThrGlnSerCys----- 819
D 2725 AAGTGCTAGCCAGCAACCTGACCCACAGACAGCCT-----CAGAAGTGGGCCCC 2778
QY 820 -----GluAspSerAspLeuAspCysPheValIle 829
D 2779 AACAGCCACTGTGAGATGGACTGCGAGGTTTAACAATGAGGACTTACTCTGTCTCATT 2838
QY 830 AspAsnAsnGlyPheIleLeuIleSerLysArgSerArg-----GluThrGlyArg 846
D 2839 GATGATGGAGAGTTCCTGGTGTCTCAACAGCAACCATCAGTGGGACAGGTGGGCAGG 2898
QY 847 PheLeuGlyGlyValValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSer 866
D 2899 TTCTTCAGTGGAGTGGATGCCACCTGATGCTGGCACTCTACAAATAACTCTCTTACACC 2958
QY 867 GlnValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisSerAla 886
D 2959 CGCAAGGAGTCTATGACTATCAGGACAGCCTGTGGCCCTCAGCCCCCTGGCAACCTGGGT 3018
QY 887 AlaGlnPro-----LeuValSerProIleSerAlaPheLeu----- 898
D 3019 GCTGCACCCCGGGGTGCTTTGTGCCACCCTGTCAGATTCTCTTAACCTGGGCTGGTG 3078
QY 899 ---ThrAlaThrArgTrpLeuLeuGlnGluValLeuPheLeuLeuGluTrpSerVal 917
D 3079 ACCTCTGCTGCCCGCTGGTCCCTGTTCACAGCAGCTTCTTACGGCTC-----ATC 3129
QY 918 TrpGlySerTrpTyrAspArgGly-----AlaGluAlaLysSerValPheHis 934
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Db 3130 TACCACAGCTGGTTCCAAAGCAGACCCCGGAGCGGAGCGGAGCGCCGAGCGCGAG 3189
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QY 955 ValTyrGlnProAlaIleArgGluAla---AsnGlyIleValGluCysGlyProCysGln 973
D 3220 ---TACTTCGGCTCGGTAAACGCTCTCTACAACGCCATCATCGACTGCGGAAACTGCTCC 3276
QY 974 LysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuValThrAsp--- 992
D 3277 AGGCTGTTCACCGCGAGACTGACCAACCAATCTTCTCTTGTGGTGGCGGAGAG 3336
QY 993 ProThrCysAspCysSerIlePheProProValLeuGlnGluAlaThrGluValLysTyr 1012
D 3337 CCCTGTGAGCCAGTCGAGGCTGCGGCTGCTGCAGAGGAGGAGGACGCTGCCACGCG 3396
QY 1013 AsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArgProAspSer 1032
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QY 1033 CysHisAlaPheHis---ProGluValArgValGluAlaAspArgGlyTrpAlaGlyPhe 1051
D 3457 TGCTTCGACTACAACCGCAGAGATACCTTCAGACTGTGGCGCGGG---GCCTCCTTC 3513
QY 1052 -----SerSerProAsnProLeuCysLeuGlyLeuCysPro 1063
D 3514 CGCCCTGCTGGCGCTCTGCTCTCCCTGCAACTGCTGCTCTCTGCGGCTCTGAGCACCTG 3573
QY 1064 CysArgGlnGluHisIleGlyMet-----ProMetAsnThr 1075
D 3574 CGSCCGCAGCCTCAAGTCTCTGTCACGCTCTCGCGCTCTGAGCACCTGCGCCACC 3633
QY 1076 ProValProVal 1079
D 3634 CCACCTCCACTC 3645

RESULT 13
US-09-397-550-19
; Sequence 19, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 5482
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-397-550-19

Alignment Scores:
Pred. No.: 2,28e-124 Length: 5482
Score: 1187.50 Matches: 348
Percent Similarity: 47.59% Conservative: 206
Best Local Similarity: 29.90% Mismatches: 429
Query Match: 20.74% Indels: 181
DB: 4 Gaps: 44

US-09-833-222A-10 (1-1090) x US-09-397-550-19 (1-5482)
QY 16 TrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLysTyrSerGlySerLeu 35
D 397 TGGGCCCCGGCTGTGGAGCAGGAGTGCAGCGGCTGATCGGATTTTGGAGGCGTCCAG 456
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Qy	36	LeuLeuGlnIysLysTyrLysAspValGlusSerSerLeuLysIleGluGluValAspGly	55
Db	457	CAGCTCGTGAGATTTTCAAGAGCAACCCGGAACTGTTCGAGGTACTCAGGAGAATGACGCT	516
Qy	56	LeuGluLeuValArgLysPheSerGluAspMetGluAenMetLeuArgAtGLyValGlu	75
Db	517	CAGAAATTGGTGGAGAAGTGGCAGGGACAATTGAGAGCCTTCTGGACAGGAAGTGCAG	576
Qy	76	AlaValGlnAenLeuValGluAlaAlaGluGluAlaAspLeuAenHisGluPheAsnGlu	95
Db	577	GCCCTGAAGAGACTGGCTGATGCTGTCAGAGAACTTCAGAAAGCACACCGTGGCAGAAC	636
Qy	96	SerLeuValPheAsp-----TyrTyraSnSerValLeuIleAenGluAgtAspGlu	112
Db	637	AACATCAAGAGGAGAGACATCGTGTACTATGACCACAAGCTGACGCTGAGCTGGACGAC	696
Qy	113	--LysGlyAsnPheValGluLeuGlyAla-----GluPheLeu	124
Db	697	CCTGAGAGTGAGGATGTGGAAGAGGGGTCTAAGGCCAGCACCTTAAGCTGGACTTCATC	756
Qy	125	LeuGluSerAenAlaHisPheSerAsnLeuProValAenThrSerIleSerSerValGln	144
Db	757	GAGACCCCAAC-----TTCAAGAAC--AAGGTCAACTATTTCATACGGCGCTGTACAG	807
Qy	145	LeuProthrAenValTyrAsnLysAspProAspIleLeuAenGlyValTyrMetSerGlu	164
Db	808	ATCCCTACGGCATCTACAAAGGCTCCACTGCTCATCTCAATGAGCTCAACTGGACAGAG	867
Qy	165	AlaLeuAenAlaValPheValGluAenPheGlnArgAspProThrLeuThrTrpGlnTyr	184
Db	868	GCCCTGAGAGATGTGTTTCATGGAAAACCGCAGACAAGACCCCAACACTGCTGTGGCAGGT	927
Qy	185	PheGlySerAlaThrGlyPhePheArgIleTyrProGlyIleLysTrpThrProAspGlu	204
Db	928	TTGGCAGCGCCACAGAGTCACTCGTACTACCCGGCCACCCCGTGGCAGAGCCCCCAAG	987
Qy	205	AsnGlyValIleThrPheAspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSer	224
Db	988	AAG---ATCGACCTGTACGATGTCGGAAGAGAGACCTGGTATATCCAGGGGGCTCGTCA	1044
Qy	225	ProLysAspIleValIleLeuValAspValSerGlySerMetLysGlyLeuArgMetThr	244
Db	1045	CCCAAAGACATGGTCATCATCGTGATGTGAGTGGCAGTGTGAGCGGCCCTGACCCCTGAAG	1104
Qy	245	IleAlaLysHisThrIleThrThrIleLeuAspThrLeuGlyGluAenAppPheValAsn	264
Db	1105	CTGATGAAGACATCTGCTCGAGATGCTGGACACGCTGCTGATGATGACTATGTGAAT	1164
Qy	265	IleIleAlaTyrAenAspTyrValHisTyrIleGluProCysPheLysGlyIleLeuVal	284
Db	1165	GTGGCCTGTTCACAGAGAGGCACACCTGTGTGTC---TGCITTCACACAC---CTGGTG	1218
Qy	285	GlnAlaAspArgAsnArgGluHisPheLysLeuLeuValGluGluLeuMetValLys	304
Db	1219	CAGGCCAATGTCGCAACAGAGAGGTGTTCAAGGAAGCTGTGACGAGCATGTTGGCCCAAG	1278
Qy	305	GlyValGlyValValAspGlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGln	324
Db	1279	GGCACCACAGCTACAGAGCGCGCTTTGAGTATGCCCTTTCACACAGCTGCAGAACTCCAAC	1338
Qy	325	GluAlaLysGlnGlySerLeuCyeAsnGlnAlaIleMetLeuIleSerAspGlyAlaVal	344
Db	1339	ATCACTCGGGCCCAAC-----TGCNACAAGATGATCATGATGTTCCAGGATGGTGGTAG	1392
Qy	345	GluAspTyrGluProValPheGluLysTyrAsnTrpProAspCysLysValArgValPhe	364
Db	1393	GACCGCTGCAGGACGCTTTTGAAGACTCAATTGGCCAAACCGCAGCGGTGCGCGTGTGT	1452
Qy	365	ThrTyrLeuIleGlyArgGluValSerPheAlaAspArgMetLysTrpIleAlaCysAsn	384
Db	1453	ACTTTCCTCCGTGGGCGACATACTATGACGTCAACCGCTGCAGTGGATGGCGCTG GCC	1512
Qy	385	AsnLysGlyTyrThrGlnIleSerThrLeuAlaAspThrGlnGluAenValMetGlu	404

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Db 2464 -----GTCTTCCCCAAACAGGAGCTGAGGAGCTGAGAGAAC 2502
Qy 733 ArgPheProLeu-----TrpTyrArgGlnAlaSerGluHisProAlaGlySerPhe 749
Db 2503 CCTGAGCCCTTCAATGCCAGCTTCTACCGCGCAGCTGGATAAC-----CACGGTTAT 2556
Qy 750 ValPheAsn-----LeuArgTrpAlaGluGlyPro---GluSer 761
Db 2557 GTCTTCAAGCCCCACACACAGGATGCCCTGTAAAG-----CCGCTGGAGCTG 2604
Qy 762 AlaGlyGluProMetValThrAlaSerThrAlaValAlaValThrValAspLysArg 781
Db 2605 GAGNATCACACTGTGGCATCTCTCGTCAGCACAGCTGTGGAGCTCAGCCTAGGACGGCG 2664
Qy 782 ThrAlaIleAlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPhe 801
Db 2665 AACTGAGGCGCAGTGTTGGGGCTCAAGCTGAGCCTAGAGGCTTGGGCTGGAGAAGTTC 2724
Qy 802 TrpAlaAlaThrArgGlnCysSerThrValAspGlyProTyrThrGlnSerCys----- 819
Db 2725 AAGGTGCTAGCCACCAACCGTACCACCAAGACGAGCT-----CAGAAGTGGCGCCC 2778
Qy 820 -----GluAspSerAspLeuAspCysPheValIle 829
Db 2779 AACGCCACTGTGAGATGGAGTGGAGGTAAACAACTAGGACTTACTCTGTCTCCTCAT 2838
Qy 830 AspAsnAsnGlyPheIleLeuIleSerLysArgSerArg-----GluThrGlyArg 846
Db 2839 GATGATGAGGATTCCTGGTGTCTCAACACAGAACCATCAGTGGGACAGGTGGGCGAG 2898
Qy 847 PheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSer 866
Db 2899 TTCTTCACTGAGTGGATGCCAACCTGATGTGGCACTCTACAATAACTCTCTTACACC 2958
Qy 867 GlnValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisSerAla 886
Db 2959 CGAAGAGGCTCTATGACTATCAGGACGCTGTGCCCTCAGCCCTCGGCAACCTGGGT 3018
Qy 887 AlaGlnPro-----LeuValSerProIleSerAlaPheLeu----- 898
Db 3019 GCTGCACCCCGGGGTGCTTTGTGGCCACCGTGGCAGATTCTTAACCTGGCGTGGTG 3078
Qy 899 ---ThrAlaThrArgTrpLeuLeuGlnGluValLeuPheLeuLeuTrpSerVal 917
Db 3079 ACCTGCTCGCGCTGCTCCCTGTTCCAGCAGCTTCTTACGCGCTC-----ATC 3129
Qy 918 TrpGlySerTrpTyrAspArgGly-----AlaGluAlaLysSerValPheHisHis 934
Db 3130 TACCACAGCTGGTTCCAAAGCAGACCCCGCGAGCGCGAGGAGCCCGCAGCGCGAG 3189
Qy 935 SerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrProValPhe 954
Db 3190 AGCAGTGCCTCATGAACAG-----ACCCAGTAC----- 3219
Qy 955 ValTyrGlnProAlaIleArgGluAla---AsnGlyIleValGluCysGlyProCysGln 973
Db 3220 ---TACTTCGGCTCGGTAAACGCCCTCTACAACGCCATCATCGACTCGGAAACTGCTCC 3276
Qy 974 LysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuValThrAsp--- 992
Db 3277 AGGCTGTTCACGCGCAGAGACTGACCAACCACTCTCTCTTTTGGTGGCGGAGAG 3336
Qy 993 ProThrCysAspCysSerIlePheProValLeuGlnGluAlaThrGluValLysTyr 1012
Db 3337 CCCTGTGACCGCTCGAGGCTGGCGGCTGTCGCAAGGAGAGCGCACTGCCCGCGC 3396
Qy 1013 AsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArgProAspSer 1032
Db 3397 GACGCCCGGAGCAGTGTGAGCTAGTCAGAGACCGCGATACCGAGAGGCCCGCACATC 3456
Qy 1033 CysHisAlaPheHis-----ProGluValArgValGluAlaAspArgGlyTrpAlaGlyPhe 1051
Db 3457 TGCTTCGACTACACCGCAGACAGATACCTCAGACTGTGGCGCGGG---GCCTCCTTC 3513
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Qy 1052 -----SerSerProAsnProLeuCysLeuGlyLeuCysPro 1063
Db 3514 CGCCCGTGGTGGCGCTCTGGTCTCCTGCAACTGCTGCTCTCTCTCTCTCTCTCTCTCT 3573
Qy 1064 CysArgGlnGluHisIleGlyMet-----ProMetAsnThr 1075
Db 3574 CGCCCGCAGGCTCAAGTCTCTGCTCCAGCCTCTCTCGCGCCTCTCTGAGCACCTCT 3633
Qy 1076 ProValProVal 1079
Db 3634 CCACCTCCACTC 3645

RESULT 14
US-09-397-550-3
; Sequence 3, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCE: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3327
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-397-550-3

Alignment Scores:
Pred. No.: 7,63e-124 Length: 3327
Score: 1179.50 Matches: 332
Percent Similarity: 48.33% Conservative: 202
Best Local Similarity: 30.05% Mismatches: 408
Query Match: 20.60% Indels: 163
DB: 4 Gaps: 40

US-09-833-222A-10 (1-1090) x US-09-397-550-3 (1-3327)
Qy 16 TrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLysTyrSerGlySerLeu 35
Db 217 TGGGCCCGCGCTCTGGAGCAGGAGTCCGAGCGGTGATCGGATTTTGTGAGGCGTCCAG 276
Qy 36 LeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIleGluGluValAspGly 55
Db 277 CAGCTCCGTGAGATTTTACAAGGACAAACCGGAACCTGTTCGAGGTACAGGAATGAGCCT 336
Qy 56 LeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgAspLysValGlu 75
Db 337 CAGAGTTGTGTGAGAAGTGGCGGGGACATTGAGAGCCTTCTGGACAGAAAGTGCAG 396
Qy 76 AlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsnHisGluPheAsnGlu 95
Db 397 GCCTTGAAGAGACTGGCTGATGCTGCAGAGAACTTCAGAAAGACACACCGCTGCGAGGAC 456
Qy 96 SerLeuValPheAsp-----TyrTyrAsnSerValLeuIleAsnGluArgAspGlu 112
Db 457 AACATCAAGGAGGAGAACACATCGTGTACTATGACGCCAAGGCTGACGCTGAGCTGGAGC 516
Qy 113 ---LysGlyAsnPheValGluLeuGlyAla-----GluPheLeu 124
Db 517 CTGAGGATGAGGATGTGAAAGGGGCTCTAAGCCGACACCTTAAGCTGGAGCTTCTATC 576
Qy 125 LeuGluSerAsnAlaHisPheSerAsnLeuProValAsnThrSerIleSerSerValGln 144
Db 577 GAGGACCCAAAC-----TTCAAGAAC---AAGGTCAACTATTTCATACGGCGGTGTACAG 627
Qy 145 LeuProThrAsnValTyrAsnLysAspProAspIleLeuAsnGlyValTyrMetSerGlu 164
Db 145 LeuProThrAsnValTyrAsnLysAspProAspIleLeuAsnGlyValTyrMetSerGlu 164
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Db 628 ATCCCTACGGACACTCTACAAGGCTCCCACTGTCTCATCTCAATGAGCTCAACTGGACAGAG 687
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Db 688 GCCTTGAGAAATGTTCATGGAAACCGCAGACAAGACCCACACTGCTGTGGCAGGTC 747
Qy 185 PheGlySerAlaThrGlyPhePheArgIleTyrProGlyIleIysTrpThrProAspGlu 204
Db 748 TTCGCAGCGCCACAGAGTCACTCGCTACTACCCGGCCACCCGCTGGCGAGCCCCAAG 807
Qy 205 AsnGlyValIleThrPheAspCysArgAsnArgGlyTrpTyrIleGlnAlaIaThrSer 224
Db 808 AAG---ATCGACCTGTACGATGTCGGAAGGAGCCCTGTGTATATCCAGGGGGCTCGTCA 864
Qy 225 ProIysAspIleValIleLeuValAspValSerGlySerMetIysGlyIleuArgMetThr 244
Db 865 CCCAAGACATGTTCATCTCGGTGATGTAGTGGCAGTGTGAGCGCCCTGACCCCTGAAG 924
Qy 245 IleAlaIysHisThrIleThrIleLeuAspThrIleuGlyGluAsnAspPheValAsn 264
Db 925 CTGATGAAGACATCTGCTCGGAGATGCTGGACACGCTGTCTGATGACTATGTGAAT 984
Qy 265 IleIleAlaTyrAsnAspTyrValHisTyrIleGluProCysPheIysGlyIleLeuVal 284
Db 985 GTGGCCTCGTTCAACGAGAGGCACAGCCTGTGTCA---TGCTTCACACAC---CTGGTG 1038
Qy 285 GlnAlaAspArgAspAsnArgGluHisPheIysLeuValGluGluLeuMetValIys 304
Db 1039 CAGGCCATGTGGCCAAAGAGGTGTTCAAGGAAGCTGTGACGGCATGTGGGCCAAG 1098
Qy 305 GlyValGlyValValAspGlnAlaLeuArgGluAlaPheGlnIleLeuIysGlnPheGln 324
Db 1099 GGCACCACAGGCTACAGGCGCGCTTGAGTATGCCTTTGACCAGCTGCAGAACTCCAAC 1158
Qy 325 GluAlaIysGlnGlySerLeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaVal 344
Db 1159 ATCACTCGGGCCAAAC---TGCAACAAGATCATCATGATTTCCAGTGTGTGTGAG 1212
Qy 345 GluAspTyrGluProValPheGluIysTyrAsnTrpProAspCysIysValArgValPhe 364
Db 1213 GACCGGTGAGGAGCGTCTTTGAGAGTACAATTGGCCAAACCGGACGGTGGCGGTGTT 1272
Qy 365 ThrTyrLeuIleGlyArgGluValSerPheAlaAspArgMetIysTrpIleAlaCysAsn 384
Db 1273 ACTTTCTCGTGGCGCAGCATACTATGACGTACACCGCTGCAGTGGATGGCTGTGCC 1332
Qy 385 AsnIysGlyTyrTyrThrGlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGlu 404
Db 1333 AACAAAGGCTACTATTTTGAATCCCTTCCATCGAGCCATCCGCATCAACACACAGGAA 1392
Qy 405 TyrLeuHisValIleuSerArgProMetValIle-----AsnHisAspIleIle 422
Db 1393 TATCTAGATGTGTGGCAGGCCCTGGTGTCTGGCAGGCAAGGAGGCCAAGAGGTTCAG 1452
Qy 423 TrpThrGluAlaTyrMetAspSerLysLeuLeuSerSerGlnAlaGlnSerIleuThrLeu 442
Db 1453 TGGACCAACGTGTATGAGAT-----GCATCGGAGCTGGGGTTG 1491
Qy 443 LeuThrThrValAlaMetProValPheSer-----LysLys 454
Db 1492 GTGTGAACAGGGACCTCCCTCGTTTTCACACCTGCACAGGATGGCCCTGGGAAAAGAAG 1551
Qy 455 AsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAspValAlaLeuArg 474
Db 1552 AACAG-----CTGATCCTGGGCGTGTGGCGATTGACCGTGGCTCTGAAT 1596
Qy 475 GluLeuMetIysLeuAlaProArgTyrLysLeuGlyValHisGlyTyrAlaPheLeuAsn 494
Db 1597 GACATCAAGAGGCTGACCCCACTACACGCTTGGAGCCAAACGGCTATGTGTTGCCATT 1656
Qy 495 ThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeu-----TyrArg 511
Db 1657 GACCTGAACGGCTACGTGTGCTGCACCCCAATCTCAAGCCCCAGACCACCACTTCCGG 1716

Qy 512 GluGlyLysIysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluValGlu 531
Db 1717 GAGCCTGTGACTCTG-----GACTTCCTGGATGGGAG 1749
Qy 532 TrpGluAspGln---AlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
Db 1750 CTAGAGATGAGAACAGGAGAGATCCCTCGGAGCATGATTGATGGCAACAAGGGCCAC 1809
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Db 1810 AAGCAGATCAGAACGTTGGTCAAGTCCCTCGATAGAGGTACATAGATGAGGTGCACACGG 1869
Qy 571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
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Qy 591 GlyHisGlyGluTyrIle----- 596
Db 1930 TACAGCACCTTCTACCTCCAAGCCAATCTCAGTGACCAGATCCTGCAGGTCAAGTATTTT 1989
Qy 597 -----LeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeuLeuHisProAsp 614
Db 1990 GAGTTCTCTCTCCCAAGCAGCTTTGAGTCTGAAGGA---CACGTTTTTCATTGCTCCAGA 2046
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Db 2047 -----GAGTACTGC---AAGGACTGTAATGCCTCAGACAACAAC 2082
Qy 635 LeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspProAsp---LeuGlu 653
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Db 2143 TGCACAACACTCTCTCTGCACAACCTGATCTTTGGACACCGGGATCAGCGAGCTGGTA 2202
Qy 673 GluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisValValAsp 692
Db 2203 GAGCGTGTGGAGGACCAAGGATCTCAAC-----ACGTACAGCCTACTG 2247
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Db 2248 GCCGTGTTTCGCTGCCACAGACGCGTGCATCAACCCGA----- 2283
Qy 713 LysValSerAspArgLysPheLeuThrProGluAlaSerValPheThrLeuAsp 732
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Qy 750 ValPheAsn-----LeuArgTrpAlaGluGlyPro---GluSer 761
Db 2377 GTCTTCAAGCCCCACACCCAGGATGCCCTGTTAAG-----COGCTGGAGCTG 2424
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Db 2425 GAGAAATGACACTGTGGGCATCTCTCGACACAGCTGTGGAGCTCAGCTAGCGAGCGC 2484
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Db 2545 AAGGTGCTAGCCAGCAACCGTACCACCAAGACCAAGCT-----CAGAAGTGGCGCCC 2598
Qy 820 -----GluAspSerAspLeuAspCysPheValIle 829
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QY 830 AspAsnAsnGlyPheIleLeuIleSerLysArgSerArg-----GluThrGlyArg 846
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Db 2659 GATGATGAGGATCTCTGGTGGTCTCAACACCAACCATCAGTGGGACCAAGGTGGCAGG 2718

QY 847 PheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSer 866
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Db 2719 TTCTTCAGTGAAGTGAATGCCAACCTGATGCTGGCACTCTACAAATACCTCTTCTACACC 2778

QY 867 GlnValThrMetTyrAspTyrGlnAlaMetCysLeysProSerSerHisHisSerAla 886
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QY 887 AlaGlnPro-----LeuValSerProIleSerAlaPheLeu----- 898
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QY 899 ---ThrAlaThrArgTrpLeuLeuGlnGluValLeuPheLeuLeuGluTrpSerVal 917
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Db 2899 ACCTCTGCTGCCGCTGGTCCCTGTTCCAGACGCTTCTTACGGCCTC-----ATC 2949

QY 918 TrpGlySerTrpTyrAspArgGly-----AlaGluAlaLysSerValPheHisHis 934
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Db 2950 TACCACAGCTGGTTCCAAAGCAGACCCCGCGAGGCGGAGGAGCCCGAGACGCGAG 3009

QY 935 SerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrProValPhe 954
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QY 955 ValTyrGlnProAlaIleArgGluAla---AsnGlyIleValGluCysGlyProCysGln 973
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QY 974 LysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuValThrAsp--- 992
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QY 993 ProThrCysAspCysSerIlePheProProValLeuGlnGluAlaThrGluValLysTyr 1012
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Db 3157 CCGCTGTGCAGCCAGTCCGAGGCTGGCGGCTGCTGCAGAAAGGAGACGCACTGCCAGCG 3216

QY 1013 AsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArgProAspSer 1032
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QY 1033 CysHisAlaPheHis 1037
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Db 3277 TGCTTCGACTACAAC 3291

RESULT 15
US-09-397-550-2
; Sequence 2, Application US/09397550
; Patent No. 6783952
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Secreted soluble alpha2 delta-2, alpha2 delta-3, alpha2
; TITLE OF INVENTION: delta-4 calcium channel subunit polypeptides and
; TITLE OF INVENTION: screening assays using same
; FILE REFERENCES: 180
; CURRENT APPLICATION NUMBER: US/09/397,550
; CURRENT FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 3248
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-397-550-2

Alignment Scores:
Pred. No.: 1,87e-121 Length: 3248
Score: 1158.50 Matches: 328
Percent Similarity: 48.30% Conservativeness: 197
Best Local Similarity: 30.17% Mismatches: 399
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Query Match: 20.23% Indels: 163
DB: 4 Gaps: 40
US-09-833-222A-10 (1-1090) x US-09-397-550-2 (1-3248)

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Db 217 TGGGCCCGCGCTGTGGAGCAGGAGGTGCGAGCGCGTGTATGCGGATTTTGGAGCGCTCCAG 276

QY 36 LeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIleGluGluValAspGly 55
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Db 277 CAGCTCCGTGAGATTTACAGGACACCGGAACCTGTTCCAGGTACAGGAGATGAGCCT 336

QY 56 LeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArgLysValGlu 75
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 337 CAGAAAGTGTGGAGAAGGTGGCAGGGGACATTTGAGAGCCTTCTGGACAGAAAGGTGCAG 396

QY 76 AlaValGlnAsnLeuValGluAlaGluGluAlaAspLeuAsnHisGluPheAsnGlu 95
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Db 397 GCGCTGAAGAGACTGGCTGATGCTGCAGAGAACTTCCAGAAACACACCCCTGGCAGGAC 456

QY 96 SerLeuValPheAsp-----TyrTyrAsnSerValLeuIleAsnGluArgAspGlu 112
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 457 AACATCAAGGAGGAGACACATCGTGTACTATGACGCCAAGGCTGACGCTGAGCTGGACGAC 516

QY 113 ---LysGlyAsnPheValGluLeuGlyAla-----GluPheLeu 124
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 517 CCTGAGAGTGAAGATGTGGAAGGGGGTCTTAAGGCCAGCACCCCTAAGGCTGGACTTCATC 576

QY 125 LeuGluSerAsnAlaHisPheSerAsnLeuProValAsnThrSerIleSerSerValGln 144
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 577 GAGGACCCAAAC-----TTCAAGAAC---AAGTCAACTATTATACGGCGCTGTACAG 627

QY 145 LeuProThrAsnValTyrAsnLysAspProAspIleLeuAsnGlyValTyrMetSerGlu 164
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Db 628 ATCCCTACCGACATCTACAAGGCTCCACTGCTCATCTCAATGAGTCAACTGACACAGAG 687

QY 165 AlaLeuAsnAlaValPheValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyr 184
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Db 688 GCGCTGGAGAATGTGTTTCATGGAAAAACCGCAGACAAGACCCACACTGCTGTGGCAGGTC 747

QY 185 PheGlySerAlaThrClyPhePheArgIleTyrProGlyIleLysTrpThrProAspGlu 204
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Db 748 TTCGGCAGCGCCACAGAGGTCACTCCGCTACTACCGGCCACCCCGTGGCGGAGCCCCCAAG 807

QY 205 AsnGlyValIleThrPheAspCysArgAsnArgGlyTrpTyrIleGlnAlaThrSer 224
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Db 808 AAG---ATCGACCTGTACGATGTCGAGGAGACCCCTGGTATATCCAGGGGCGCTCGTCA 864

QY 225 ProLysAspIleValIleLeuValAspValSerGlySerMetLysGlyLeuArgMetThr 244
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
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QY 245 IleAlaLysHisThrIleThrIleLeuAspThrLeuGlyGluAsnAspPheValAsn 264
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Db 925 CTGATAAAGACATCTCTCTCGAGAGTGTGGACACGCTGTCTGATGATGATGATGTAAT 984

QY 265 IleIleAlaTyrAsnAspTyrValHisTyrIleGluProCysPheLysGlyIleLeuVal 284
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Db 985 GTGGCCTCGTTCAACGAGAAGGACACAGCCTGTGTCA---TGCTTTCACACAC---CTGGTG 1038

QY 285 GlnAlaAspArgAspAsnArgGluHisPheLysLeuLeuValGluGluLeuMetValLys 304
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 1039 CAGGCCAATGTGCGCAACAAGAGGTGTTCAAGGAAGCTGTGAGGGGCGCATGGTGGCCAAAG 1098

QY 305 GlyValGlyValValAspGlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGln 324
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Db 1099 GGCACCAAGGCTACAAGGCCGCTTTGAGTATGCTTTTGACCACGCTGCAGAACTCCAAC 1158

QY 325 GluAlaLysGlnGlySerLeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaVal 344
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 1159 ATCACTCGGGCCCAAC-----TGCAACAAGATGATCATGATGTTACGGATGTTGGTGAG 1212
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345 GluAspTyrGluProValPheGluLysTyrAsnTrpProAspCysLysValArgValPhe 364
 1213 GACCGCTGGCAGGACGCTTTTGGAGAGTCACAATTTGGCCAAACCGGACGGTGGCGTGT 1272
 365 ThrTyrLeuIleGlyArgGluValSerPheAlaAspArgMetLysTrpIleAlaCysAsn 384
 1273 ACTTTCCTGGTGGGCGAGCATAACTATGACGTCAACCGCTGCGAGTGGATGGCGCTGTGCC 1332
 385 AsnLysGlyTyrTyrThrGlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGlu 404
 1333 AACAAAGCTACTATTTTGGATCCCTTCCATCGGAGCCATCCGCATCAACACACAGGAA 1392
 405 TyrLeuHisValLeuSerArgProMetValIle-----AsnHisAspHisAspIleIle 422
 1393 TATCTAGATGTGTGGCAGGCCCATCGTGTGGCAGCAAGGAGGCAACAGCAGGTTTCAG 1452
 423 TrpThrGluAlaTyrMetAspSerLysLeuLeuSerSerGlnAlaGlnSerLeuThrLeu 442
 1453 TGGACCAACGTGTATGAGGAT-----GCATGGGACTGGGGGTG 1499
 443 LeuThrTrpValAlaMetProValPheSer-----LysLys 454
 1492 GTGGTAACAGGACCCCTCCCTGTTTCACTGCACAGGATGCCCTGGGGAAAGAAG 1551
 455 AsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAspValAlaLeuArg 474
 1552 AACCA-----CTGATCTGGGCGTGTGGCATTTGACGTGGCTCTGAAAT 1596
 475 GluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyrAlaPheLeuAsn 494
 1597 GACATCAAGAGGCTGACCCCAACTACACGCTTGGAGCAACGCTATGTGTGCCAAT 1656
 495 ThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeu-----TyrArg 511
 1657 GACCTGAACGGCTACGTTGTCTGCCACCCCAATCTCAAGCCCCAGACCACCACTTCCGG 1716
 512 GluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluValGlu 531
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 532 TrpGluAspGln---AlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
 1750 CTAGAGATGAGAACCAAGGAAGAGATCCGTGGAGCATGATTGATGSCAACAAAGGGCCAC 1809
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 1810 AAGCAGATCAGAACGTTGGTCAAGTCCCTCGATGAGAGGTACATAGTAGGATGACACCG 1869
 571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
 1870 AACTACACCTGGGTGCCTATAAGAGGACACTAACTACAGCCTGGGGTGGTGTCTCCACCC 1929
 591 GlyHisGlyGluTyrIle----- 596
 1930 TACAGCACCTTCTACCTTCCAAGCCAACTCTCAGTGACCGATCTCTGCAGGTCAAGTATTTT 1989
 597 -----LeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeuLeuHisProAsp 614
 1990 GAGTTCTGTCTCCAGCAGCTTTGAGTCTGAAGGA---CACGTTTTCATTGCTCCACAGA 2046
 615 LeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspProAspHisArgLys 634
 2047 -----GAGTACTGC--AAGGACCTGAATGCCTCAGACACAACAAC 2082
 635 LeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspProAsp-----LeuGlu 653
 2083 ACCGAGTTCTGAAACATTTTATTTGAGCTCATGGAGAAAGTGACTCCAGACTCCAAGCAG 2142
 654 CysAspGluGluLeuValArgGluValPheAspAlaValValThrAlaProMet--- 672
 2143 TGCACAACTTCCTCTGCGCAACCTGTGATCTTGACACAGGGGCATCAGCAGCAGCTGGTA 2202
 673 GluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisValValAsp 692

[illegible]

Db 3157 CCGCTGTGCAGCCAGTCGAGGCTGGCCGCTGCTGCAGAAAGGAGACGCCACTGCCACGCG 3216
Qy 1013 AsnAlaSerVallysCysAsp 1019
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Job time : 602 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 16, 2005, 22:05:05 ; Search time 8018 Seconds
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Scoring table: BLOSUM62
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Fgapop 6.0 , Fgapext 7.0
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Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Database :

EST:*

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2	2591	45.2	2690	9 AY404366	AY404366 Mus muscu
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5	1800.5	31.4	3230	3 AK044427	AK044427 Mus muscu
6	1356	23.7	916	3 BF1518624	BF1518624 603061574
7	1317.5	23.0	892	1 AL558158	AL558158 AL558158
8	1297	22.7	1446	3 CR603629	CR603629 full-leng
9	1266	22.1	747	6 CD743170	CD743170 UI-H-Ftl-

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

10	1246.5	21.8	853	4	BI908421	BI908421 603067367
11	1228	21.4	765	7	CO424223	CO424223 UI-M-HU0-
12	1208	21.1	940	5	BQ193363	BQ193363 AGENCOURT
13	1182.5	20.7	777	4	BI908463	BI908463 603069223
14	1180	20.6	3527	3	AK044603	AK044603 Mus muscu
15	1157.5	20.2	725	4	EG436760	EG436760 602489181
16	1136	19.8	942	5	BU155034	BU155034 AGENCOURT
17	1130	19.7	776	7	CNS39658	CNS39658 UI-M-HU0-
18	1107	19.3	764	4	BI906089	BI906089 603062468
19	1092.5	19.1	946	5	BU749673	BU749673 CH3#028 C
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22	1029	18.0	893	6	CD513443	CD513443 AGENCOURT
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24	974	17.0	842	6	CD107126	CD107126 AGENCOURT
25	936.5	16.7	688	4	BI871869	BI871869 603396817
26	936.5	16.4	601	2	BE276523	BE276523 601144143
27	931	16.3	794	7	CK130243	CK130243 AGENCOURT
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29	927	16.2	779	7	CK130239	CK130239 AGENCOURT
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32	901.5	15.7	2791	9	AY403434	AY403434 Homo sapi
33	898.5	15.7	852	5	BX329163	BX329163 BX329163
34	897.5	15.7	2730	9	AY403436	AY403436 Mus muscu
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37	866	15.1	819	5	BU747580	BU747580 CH3#013 G
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ALIGNMENTS

RESULT 1

LOCUS AY404364

DEFINITION Homo sapiens CACNA2D3 gene, VIRTUAL TRANSCRIPT, partial sequence,

genomic survey sequence.

ACCESSION AY404364.1 GI:39760341

VERSION AY404364.1

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2730)

AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarial,A., Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 2730)

AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarial,A., Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

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Score:	2593.50	Matches:	487		
Percent Similarity:	70.78%	Conservative:	155		
Best Local Similarity:	53.69%	Mismatches:	248		
Query Match:	45.29%	Indels:	18		
DB:	9	Gaps:	7		
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Db	61	TTTGACCGTGACCCATCTCTCATATGGCAGTACTTTTGGAAAGTGCAAAGGGCTTTTATAGG	120	NN	960
Qy	194	IleTyrProGlyIleLysTrpThrProAspGluAenGlyValIleThrPheAspCysArg	213	ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr	490
Db	121	CAGTATCCGGGGATTAATCGGAACCCAGATGAGAATGGAGTCATTGCTTCGACTCGAGG	180	GTCCCAAGTAAAGAACTTCTGAAGACCATCCCAAAATACAAGTTAGGATTACCGGTAT	1020
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Qy	234	ValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThrThrIle	253	ArgGluGlyLysLysProLysProAsnTyrAsnSerValAspLeuSerGluVal	530
Db	241	GTGAGTGGCAGCATGAAGGACTCCGTCTGACTATCGCGAAGCAACAGTCTCATCCATT	300	GAAGAAGGAAAGAG--CGAAGGAACCTTAATATAGTAGCCTTGACCTCTCTGAGGTG	1137
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Db	301	TTGGATACACTTGGGATGATGACTTCTTCAACATAATTTGCTTATATAGGAGCTTCAC	360	GAGTGGGAAGACCGAGATGACGTGCTGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	1197
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Db	361	TATGTGGAACCTTGCTGTAATGGAACTTTGTGCAAGCCGACAGCAACAAAGAGCAC	420	NNNNCCATGGAGGTGAAGAAGACAGTGGCAAGGGAAACGGGTTTGGTGTAGTACAAAT	1257
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Qy	314	ArgGluAlaPheGlnIleLysGlnPheGlnGluAlaLysGlnGlySerLeuCysAen	333	GlyHisGlyGluTyrIleLeuLeuGlyAenThrSerValGluGluGlyLeuHisAspLeu	610
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Qy	334	GlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProValPheGluLys	353	LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro	630
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Db	781	GTATCGACGAGGAGCATGATGGTGTGGACCGGAACTTACATTTGACAGCANNNNNNNN	840	GTGGAGTTGCTCTCTCGGCATCGACGGGCTTCCAGAAATCAACCTGTTTGTGCGGG	1677

Qy	354	TyrAenTrpProAspCysLysValargValPheThrTyrLeuIleGlyArgGluValSer	373
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Qy	471	ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrIlysLeuGlyValHisGlyTyr	490
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Qy	511	ArgGluGlyLysLysLeuLysProLysProAenTyrAenSerValAspLeuSerGluVal	530
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Qy	611	LeuHisProAspLeuAlaLeuAlaGlyAspTpIleTyrCysIleThrAspIleAspPro	630
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DEFINITION      sequence, genomic survey sequence.
ACCESSION      AY404365
VERSION      AY404365.1 GI:39760342
KEYWORDS      GSS.
SOURCE      Pan troglodytes (chimpanzee)
ORGANISM      Pan troglodytes
REFERENCE      1 (bases 1 to 2730)
AUTHORS      Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
      Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
      Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
      Adams,M.D. and Cargill,M.
TITLE      Inferring nonneutral evolution from human-chimp-mouse orthologous
      gene trios
JOURNAL      Science 302 (5652), 1960-1963 (2003)
PUBMED      14671302
REFERENCE      2 (bases 1 to 2730)
AUTHORS      Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
      Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
      Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
      Adams,M.D. and Cargill,M.
TITLE      Direct Submission
JOURNAL      Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
      Rockville, MD 20850, USA
COMMENT      This sequence was made by sequencing genomic exons and ordering
      them based on alignment.
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ORIGIN

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Percent Similarity:      68.25%      Conservative:      146
Best Local Similarity:      52.15%      Mismatches:      271
Query Match:      43.55%      Indels:      18
DB:      9      Gaps:      7

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Qy      571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
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Qy      611 LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630
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Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saich, R., Saich, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayaishizaki, Y.

TITLE

Submitted (16-JUL-2001) Yoshihide Hayaishizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/

FEATURES

source

1. .2583
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="PANTOM_DB:5730412N02"
/db_xref="taxon:10090"
/clone="5730412N02"
/tissue_type="whole body"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="8 days embryo"

misc_feature

1. .2583
/note="hypothetical von Willebrand factor type A domain containing protein (InterPro|IPR002035, evidence: InterPro)"

ORIGIN

Alignment Scores:

Pred. No.: 1.14e-231 Length: 2583
Score: 2241.00 Matches: 422
Percent Similarity: 95.64% Conservative: 17
Best Local Similarity: 91.94% Mismatches: 20
Query Match: 39.14% Indels: 0
DB: 3 Gaps: 0

US-09-833-222A-10 (1-1090) x AK030723 (1-2583)

Qy 197 GlyIleLysTrpThrProAspGluAsnGlyValIleThrPheAspCysArgAsnArgGly 216
Db 215 GGAATAAGTGGATGCTGATGAAGAAGGATCATCGCTTCGACTCGAGNAACCGTGGC 274
Qy 217 TrpTrpIleGlnAlaThrSerProLysAspIleValIleLeuValAspValSerGly 236
Db 275 TGGTACATACAAAGTGCACATCTCCCAAGACATCGTAATTCGTGGATGATGCGGC 334
Qy 237 SerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThrIleLeuAspThr 256
Db 335 AGCATGAAGGGCGGTGAGATGGCTATCGCAAGCACACCATATACCATATTCGACAC 394
Qy 257 LeuGlyGluAsnAppPheValAsnIleAlaTrpAsnAspTrpValHisTrpIleGlu 276
Db 395 CTGGAGGAAACGACTTCGTGAACATCATCGGTACATGATGATGATGATGATGATGAT 454
Qy 277 ProCysPheLysGlyIleLeuValGlnAlaAspArgAsnArgGluHisPheLysLeu 296
Db 455 CCCTGCTTCAAGGATCTTGTCCAGCAGATCGAGACACCGAGAGCATTTCAAGCAG 514
Qy 297 LeuValGluGluLeuMetValLysGlyValGlyValValAspGlnAlaLeuArgGluAla 316
Db 515 TTGGTGGATGAGCTGATGGTCAAAAGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT 574

RESULT 5

AK044427

LOCUS

DEFINITION

AK044427 3230 bp mRNA linear HTC 03-APR-2004
Mus musculus adult retina cDNA, RIKEN full-length enriched library.

Qy 317 PheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySerLeuCysAsnGlnAlaIle 336
Db 575 TTCGAGATCTGAAACAGTTCCAAAGAGTCCAAACAGGAAGTCTCTCTCAACACCGCCATC 634
Qy 337 MetLeuIleSerAspGlyAlaValGluAspTrpGluProValPheGluLysTrp 356
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Qy 357 ProAspCysLysValArgValPheThrTrpLeuIleGlyArgGluValSerPheAlaAsp 376
Db 695 CAGACCGAAAGGTCCGAGTTTTCACCTTATTCGAAAGAGAGTGTCTTCGCTGAC 754
Qy 377 ArgMetLysTrpIleAlaCysAsnAsnLysGlyTrpTrpThrGlnIleSerThrLeuAla 396
Db 755 CGCATGAAGTGGATCGCTGCCAACATAAAGGCTACTACACACAGATCTCCACACTGGCG 814
Qy 397 AspThrGlnGluAsnValMetGluTrpLeuHisValLeuSerArgProMetValIleAsn 416
Db 815 GATGCGCAGAGAGCGGTGATGGAGTACTCTGATGTGCTTAGCCGCCCATCGTATCAAC 874
Qy 417 HisAspHisAspIleIleTrpThrGluAlaTrpMetAspSerLysLeuSerSerGln 436
Db 875 CATGACCCACATCATCTCGACAGAGCTTACATGACAGCCGGCTCTTCCACATCAGAG 934
Qy 437 AlaGlnSerLeuThrLeuLeuThrValAlaMetProValPheSerLysLysAsnGlu 456
Db 935 GCACAGAGCTGATGCTCTCCACACAGTGGCCATGCTGTCTTCAGCAAAAGATGAA 994
Qy 457 ThrArgSerHisGlyIleLeuLeuGlyValValGlySerAspValAlaLeuArgGluLeu 476
Db 995 ACAAGATCCCATGGCATCTCCCTGGGTGTAGTGGCTCTGACGTGACCTTAAGAGAGCTC 1054
Qy 477 MetLysLeuAlaProArgTrpLysLeuGlyValHisGlyTrpAlaPheLeuAsnThrAsn 496
Db 1055 ATGAGCTGGCACCCCGATATAGCTTGGGTGATGCTGCTCTTCTTGAACACTAAC 1114
Qy 497 AsnGlyTrpIleLeuSerHisProAspLeuArgProLeuThrLeuSerMetAspValLys 516
Db 1115 AATGGCTACATCTCTCTCATCTCGACTCGACCTTGTACAGAGAAGCAAGAGCTG 1174
Qy 517 LysProLysProAsnTrpAsnSerValAspLeuSerGluValGluTrpGluAspGlnAla 536
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Qy 557 ValProMetAspLysGlyLysArgValLeuPheLeuThrAsnAspTrpPhePheThrAsp 576
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Qy 577 IleSerAspThrProPheSerLeuGlyAlaValLeuSerArgGlyHisGlyLysTrpIle 596
Db 1355 ATCAGTGCACACCTTTTCAGCTGGAGTGGTGTCTCACCAGAGGTCTATGGAGAATACATC 1414
Qy 597 LeuLeuGlyAsnThrSerValGluGlyLeuHisAspLeuLeuHisProAspLeuAla 616
Db 1415 CTCTGGGGAACACATCTGTGGAAGAGGCTGACCGACTTGTCTTCCGATCTGACC 1474
Qy 617 LeuAlaGlyAspTrpIleTrpCysIleThrAspIleAspProAspHisArgLysLeuSer 636
Db 1475 CTGGCCAGTGCATGATCTACTGTATCACAGATATCGACCGGACCCCGGAAATCTCAGC 1534
Qy 637 GlnLeuGluAlaMetIleArgPheLeuThrArgLysAspProAspLeuGluCysAsp 655
Db 1535 CAATGGAGCTGTGGTTCGTCTCTCAGAGGGGTGGATCCAGACCTGGAGTGTGAG 1591

clone:A930012E17 product:hypothetical von Willebrand factor type A domain containing protein, full insert sequence.

ACCESSION
AK044427

VERSION
AK044427.1 GI:26090352

KEYWORDS
HTC; CAP trapper.

SOURCE
Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Method. Enzymol. 303, 19-44 (1999)

99279253

PUBMED

10349636

REFERENCE

2 Carninci, P., Shibata, K., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

20499374

PUBMED

11042159

REFERENCE

AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

20530913

PUBMED

11076861

REFERENCE

AUTHORS

4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

REFERENCE

AUTHORS

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

6 (bases 1 to 3230)

Nature 420, 563-573 (2002)

6 (bases 1 to 3230)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saitoh, H., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

81-45-503-9216

81-45-503-9216

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

COMMENT

Retina RNA was provided by Dr. Stefano Guatincich (Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA 02115, USA) whose assistance is gratefully acknowledged. Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.

FEATURES

source

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Location/Qualifiers
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/strain="C57BL/6J"
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/clone="A930012E17"
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1..3230
/notes="hypothetical von Willebrand factor type A domain containing protein (InterPro|IPR002035, evidence: InterPro)"

ORIGIN

Alignment Scores:
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Percent Similarity: 43.67% Conservative: 24
Best Local Similarity: 41.18% Mismatches: 21
Indels: 523
Query Match: 31.44% Gaps: 1
DB: 3
US-09-833-222A-10 (1-1090) x AK044427 (1-3230)
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Db 340 GAAACAGTGAAGCTGTGGCCGATACCTTCGGCAGGAATCTGTACACACGGTGACCAGA 399
Qy 31 TyrSerGlySerLeuLeuLeuGlnLysLysValLysAspValGluSerSerLysIle 50
Db 400 TATTCAGGCTCCCTCTCTGTCGAGAGAGATGACAGGATGCAGAACCCAGTCTGAAGATC 459
Qy 51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAenMetLeu 70
Db 460 AAAAGAGTGGATGGCTGTGGAGCTGTGGAAGAGTTCGCGAGGACATGGAGACCATGCTT 519
Qy 71 ArgArgLysValGluAlaValGlnAenLeuValGluAlaAlaGluGluAlaAspLeuAen 90
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Qy 91 HisGluPheAenGluSerLeuVal----- 98
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Qy 98 ----- 98
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Qy 98 ----- 98
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Qy 98 ----- 98
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Qy 98 ----- 98
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Qy 98 ----- 98
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Qy 98 ----- 98

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Qy 109 GluArgAspGluLysGlyAenPheValGluLeuAlaGluPheLeuLeuGluSerAen 128
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Qy 129 AlaHisPheSerAenLeuProValAenThrSerIleSerSerValGlnLeuProThrAen 148
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Qy 209 ThrPheAspCysArgAenArgGlyTyrTrpTyrIleGlnAlaAlaThrSerProLysAspIle 228
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Qy 449 ProValPheSer 452
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RESULT 6
BI518624 916 bp mRNA linear EST 29-AUG-2001
LOCUS 603061574F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5210826 5',
DEFINITION mRNA sequence.
ACCESSION BI518624
VERSION BI518624.1 GI:15343416
SOURCE EST.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 916)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM1529 row: c column: 19
High quality sequence stop: 842.

FEATURES
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(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."

ORIGIN
Alignment Scores: 4.19e-136 Length: 916
Pred. No.: 1356.00 Matches: 261
Score: 88.89% Conservative: 3
Percent Similarity: 87.88% Mismatches: 14
Best Local Similarity: 23.68% Indels: 19
Query Match: 4
DB: Gaps: 1

US-09-833-222A-10 (1-1090) x BI518624 (1-916)

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RESULT 7
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DEFINITION Homo sapiens cDNA clone CS0DJ001YM12 5-PRIME, mRNA sequence.
ACCESSION AL558158
VERSION AL558158.3 GI:46183556
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 892)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:31279957.
Contact: Genoscope
Genoscope - Centre National de Sequençage
```

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 6520.r.
 and it belongs to a clone representative of this cluster. For more
 information about this cluster and the virtual cDNA, see
 http://www.genoscope.cns.fr/cdna?c=CS0DJ001BG06QPI&c=6520.r.

FEATURES

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 10-NORMALIZED"
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 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and EcoR V sites of the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred No.: 6, 21e-132 Length: 892
 Score: 1317.50 Matches: 252
 Percent Similarity: 92.39% Conservative: 3
 Best Local Similarity: 91.30% Mismatches: 18
 Query Match: 23.01% Indels: 3
 DB: 1 Gaps: 2

US-09-833-222A-10 (1-1090) x AL558158 (1-892)

Qy 789 GlyValGlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCys 808
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 Qy 809 SerThrValAspGlyProTyThrGlnSerCysGluAspSerAspLeuAspCysPheVal 828
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 Qy 829 IleAspAsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyValArgPheLeu 848
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 Qy 849 GlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnVal 868
 Db 183 GGGGAGGTGGATGGTGTCTCTGACCCAGCTGCTCAGCATGGGGTGTTCAGCCAAAGTG 242
 Qy 869 ThrMetTyrrAspTyrrGlnAlaMetCysLysProSerSerHisHisSerAlaAlaGln 888
 Db 243 ACTATGTATGACTATCAGGCCATGTGCAAAACCCCTCGAGTCCACACAGTGCAGCCAG 302
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 Db 357 GTGCTGTTCTCTGCTGGAGTGGAGTGTCTGGGGCTCTCTGGTACGACAGAGGGCGCAGGCC 416
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 Qy 949 ThrGluTyrrProValPheValTyrrGlnProAlaIleArgGluAlaAsnGlyIleValGlu 968
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 Db 774 SCTCGGACACCTCAGCTCGCGCCCTACTCCYCGCTGCTGTGT 821
 RESULT 8
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 LOCUS
 DEFINITION
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 Cot 10-normalized of Homo sapiens (human).
 ACCESSION
 CR603629.1 GI:50484436
 VERSION
 CR603629.1
 KEYWORDS
 HMC; CNSLT cDNA.
 SOURCE
 Homo sapiens
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 1446)
 AUTHORS
 Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
 TITLE
 Full-length cDNA libraries and normalization
 JOURNAL
 Unpublished
 REMARK
 Contact : feng liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ invitrogen Corporation 1600
 Faraday Avenue
 REFERENCE
 2 (bases 1 to 1446)
 AUTHORS
 Genoscope.
 TITLE
 Direct Submission
 JOURNAL
 Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr)
 COMMENT
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
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 /tissue_type="T cells (Jurkat cell line) Cot
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 /plasmid="pCMVSPORT_6"
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 Score: 1297.00 Matches: 255
 Percent Similarity: 89.66% Conservative: 5
 Best Local Similarity: 87.93% Mismatches: 26
 Query Match: 22.65% Indels: 6
 DB: 3 Gaps: 2
 US-09-833-222A-10 (1-1090) x CR603629 (1-1446)
 Qy 789 GlyValGlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCys 808

Db	3	GGCTCCAAATGAAGCTGAATTCCTCAGCGCAAAATTCGGGCGGCAACGCGCAGTGC	62
Qy	809	SerThrValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheVal	828
Db	63	AGCACTGTGGATGGCGCTGCACACAGCTGCCAGGACAGTGAATCTGGCTTCGTC	122
Qy	829	IleAspAenAenGlyPheIleLeuIleSerIysArgSerArgGluThrGlyArgPheLeu	848
Db	123	ATCGACAAACACGGTTTCATCTCTATCTCCAAAGAGTCCCGAGAGACGGGAAGATTTCG	182
Qy	849	GlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnVal	868
Db	183	GGGAGGTGGATGCTGCTCTCACCAGCTGCTAGCATGGGGGTGTTTCAGCCAAAGTG	242
Qy	869	ThrMetTyrAspTyrGlnAlaMetCysIysProSerSerHisHisHisSerAlaAaGln	888
Db	243	ACTATGATGACTATACAGCCATGTGCAAAACCTTCGAGTCACCAACAGTGCAGCCAG	302
Qy	889	ProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeu	908
Db	303	CCCTCG-----CCAAATTCCTGCTTCTGACGGCGACAGGTGGCTGCTGCAGGAGCTG	356
Qy	909	ValLeuPheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAla	928
Db	357	GTGCTGTCTCTGGAGTGGAGTGTCTGGGGCTCTCTGTGTACGACAGGGGGCGGAGCC	416
Qy	929	LysSerValPheHisHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAsp	948
Db	417	ANAAAGTGTCTTCATCTCCCAACACAAAGAGCAGGACCCGCTGCAGCCCTGGGAC	476
Qy	949	ThrGluTyrProValPheValTyrGlnProAlaIleArgGluAlaAenGlyIleValGlu	968
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Qy	969	CysGlyProCysGlnLysValPheValValGlnGlnIleProAenSerAenLeuLeu	988
Db	537	TGGGGGCCCCGCCAAGAGGATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	596
Qy	989	LeuValThrAspProThrCysAspCysSerIlePheProValLeuGlnGluAlaThr	1008
Db	597	CTGGTGACAGACCCACCTGTGACTGTGAGCATCTTCCACAGTGTGTGTGTGTGTGTGT	656
Qy	1009	Glu-----ValIysTyrAenAlaSerValLysCysAspArgMetArgSerGlnLysLeu	1026
Db	657	GAATGGCTTCGCA-CATAATGCTCTGTCAATGTGACCGGATGGCTCCAGAGAGCTC	715
Qy	1027	ArgArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspArg	1046
Db	716	CGCGGGCGACCACTCTCTGCCAGCGCTTCCATCCAGAGGAATGCCAGGACTGCGGC	775
Qy	1047	GlyTrpAlaGlyPheSerSerProAenProLeuCysLeuGlyLeuCysProCysArgGln	1066
Db	776	GGGCGCTCGACACCTCAGCTGCGCGCCCTACTCTCTGTCT-GCTGTGTGTGTGTGTGT	834
Qy	1067	GluHisIleGlyMetProMetAenThrPro 1076	
Db	835	GCTACTGCCCAACTCTCGGT	864
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LOCUS	CD743170/c	747 bp	mRNA
DEFINITION	UI-H-FTI-bkc-o-08-0-UI.s1	NCI CGAP_FTI	linear
VERSION	CD743170	EST	05-AUG-2004
KEYWORDS	CD743170.1	GI:3294020	
SOURCE	EST.		
ORGANISM	Homo sapiens		
REFERENCE	1	(bases 1 to 747)	
AUTHORS	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		

JOURNAL	Tumor Gene Index
COMMENT	Unpublished (1997)
	Contact: Daniela S. Gerhard, Ph.D.
	Office of Cancer Genomics
	National Cancer Institute / NIH
	Bldg. 31 Rm10A07 Bethesda, MD 20892
	Email: cgaps-r@mail.nih.gov
	CDNA Library preparation: Dr. Gary W. Hunninghake, U of I
	CDNA sequencing by: Dr. M. Bento Soares, University of Iowa
	Clone Distribution: Distribution information can be found at
	http://genome.uiowa.edu/distribution/cgap.html
	The following repetitive elements were found in this CDNA
	sequence: 183-231, >HERV#LIR/Retroviral
	Seq primer: M13 FORWARD
	POLYA=Yes.
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	/dev_stage="Adult"
	/lab_host="DH10B (Life Technologies)"
	/clone_lib="NCI_CGAP_FTI1"
	/notes="Organ: Lung; Vector: p773-Pac (Pharmacia) with a
	modified polylinker; Site 1: EcoR I; Site 2: Not I;
	NCI_CGAP_FTI1 is a normalized CDNA library constructed from
	a pool of 81 RNA samples from Alveolar Macrophages
	challenged with different treatments. The mRNA samples
	were a mixture of these conditions (times refer to
	incubations following isolation by bronchoalveolar lavage)
	(some normal donor macrophages were cultured in some of
	the conditions, other donor macrophages in different
	conditions). The mRNA samples were pooled for library
	construction. Control 0 hours; control 3 hours; control 24
	hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
	PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
	moi 10, 3 hours; Staph aureus moi 10, 24 hours; Staph aureus
	vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector
	(Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,
	3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
	3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
	hours; wt adenovirus + LPS 24 hours. The library was
	normalized according to Bonaldo, Lennon and Soares, Genome
	Research, 6:791-806, 1996. First strand cDNA synthesis was
	primed with an oligo-dT primer containing a Not I site.
	Double stranded cDNA was ligated to an EcoR I adaptor,
	digested with Not I, and cloned directionally into
	p773-Pac vector. The oligonucleotide used to prime the
	synthesis of first-strand cDNA contains a library tag
	sequence that is located between the Not I site and the
	(dT)18 tail. The sequence tag for this library is
	GGCCATGCCG. The tissue was provided by Dr. Gary W.
	Hunninghake of the University of Iowa.
	TAG_TISSUE=Human Lung Alveolar Macrophage
	TAG_LIB=UI-H-FTI
	TAG_SEQ=GGCCATGCCG"
ORIGIN	
Alignment Scores:	
Pred. No.:	1.85e-126
Score:	1266.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	22.11%
DB:	6
	Length: 747
	Matches: 231
	Conservative: 0
	Mismatches: 0
	Indels: 0
	Gaps: 0
	US-09-833-222A-10 (1-1090) x CD743170 (1-747)

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 Qy 880 SerSerHisHisSerAlaGlnProLeuValSerProIleSerAlaPheLeuThr 899
 Db 687 TCGAGTCACACACACAGTCAGAGCCCGCTGGTCAGCCCAATTTCTGCCCTTTGACG 628
 Qy 900 AlaThrArgTrrpLeuLeuGlnGluLeuValLeuPheLeuLeuGluTrrpSerValTrpGly 919
 Db 627 CGCAGCAGGTGGCTGCTCAGGAGCTGGTGTCTTCTGCTGAGTGAGTGTCTGGGCG 568
 Qy 920 SerTrrpTyrAspArgGlyAlaGluAlaLysSerValPheHisHisSerHisLysHisLys 939
 Db 567 TCCTGGTACGACAGAGGGCGGAGCCCAAAAGTGTCTTCCATCACTCCCAACAAACAAG 508
 Qy 940 LysGlnAspProLeuGlnProCysAspThrGluTrrpProValPheValTyrGlnProAla 959
 Db 507 AAGCAGGACCGCTGCAGCCCTGGACACGAGGTACCCCGTGTCTGTACCAACCCGCCC 448
 Qy 960 IleArgGluAlaAanGlyIleValGluCysGlyProCysGlnLysValPheValValGln 979
 Db 447 ATCCGGGAGGCCAACGGGATCGTGGAGTGGCGGCCCTGCCAGAGGTATTTGTGGTGCAG 388
 Qy 980 GlnIleProAanSerAanLeuLeuLeuValThrAspProThrCysAspCysSerIle 999
 Db 387 CAGATTCCCAACAGTAACCTCTCTCTCTGTGTGACAGACCCACCTGTGACTGCAGCATC 328
 Qy 1000 PheProProValLeuGlnGluAlaThrGluValLysTyrAanAlaSerValLysCysAsp 1019
 Db 327 TTCCACCAAGTCTGCAGGAGCGACAGAGTCAATATATATGCTCTGTCAATGTGAC 268
 Qy 1020 ArgMetArgSerGlnLysLeuArgArgProAspSerCysHisAlaPheHisProGlu 1039
 Db 267 CGGATCGCTCCCAAGAGCTCCGCGCGGACAGACCTCTGCCACCGCTTCCATCCAGAG 208
 Qy 1040 ValArgValGluAlaAspArgGlyTrrpAlaGlyPheSerSerProAanProLeuCysLeu 1059
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 Qy 1060 GlyLeuCysProCysArgGlnGluHisIleGlyMetProMetAanThrProValProVal 1079
 Db 147 GGTCTGTGCGCCCTGCACAGAGGAGCATATAGGATGCCAATGAACACACCTGTGCCCTGTG 88
 Qy 1080 LeuLeuGlyGlyAenIleArgValTyrAlaLeu 1090
 Db 87 CTTCCTGGGGGAACATTCGGGTTTATGCCCTG 55

RESULT 10
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 LOCUS 603067367F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5216273 5',
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 ACCESSION B1908421
 VERSION B1908421.1 GI:16171373
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 853)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: csapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: LLAM1543 row: f column: 18
 High quality sequence stop: 841.
 Location/Qualifiers
 source 1..853

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 /clone="IMAGE:5216273"
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 /clone_lib="NIH_MGC_118"
 /note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV
 (destroyed); RNA source leukocytes from anonymous pool of
 non-activated adult donors. Library is oligo-dT primed
 and directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.7 kb, insert size range
 1.2-3.3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 027. Note:
 this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
 Pred. No.: 3,08e-124 Length: 853
 Score: 1246.50 Matches: 247
 Percent Similarity: 87.32% Conservative: 1
 Best Local Similarity: 86.97% Mismatches: 13
 Query Match: 21.77% Indels: 23
 DB: 4 Gaps: 3

US-09-833-222A-10 (1-1090) x B1908421 (1-853)

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 Db 94 CAG-----GATCTGGACTGC 108
 Qy 827 PheValIleAspAanGlyPheIleLeuIleSerLysArgSerArgGluThrGlyValArg 846
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 Db 349 GAGCTGGTCTGTCTCTGCTGGAGTGGAGTGTCTGGGGCTCTCTGTGTACGACAGAGGGGCC 408
 Qy 927 GluAla-LysSerValPheHisSerHisLysHisLysLysGlnAspProLeuGlnPr 946
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Qy 1046 rgGlyTTPAlaGlyPheSerSerProAsnProLeu-----CysLeuGlyL 1061
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Qy 1061 euCysPro 1063
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RESULT 11
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IMAGE:30666472 5', mRNA sequence.
CO424223
CO424223.1 GI:49670350
EST.
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 765)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5.
Location/Qualifiers
1. 765
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Site 2: Not I; The library was constructed according
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AATAATTACG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."

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FEATURES

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Site 2: Not I; The library was constructed according
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dt
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AATAATTACG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."

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ORIGIN

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Alignment Scores:
Pred. No.: 2,64e-122 Length: 765
Score: 1228.00 Matches: 233
Percent Similarity: 95.29% Conservative: 10
Best Local Similarity: 91.37% Mismatches: 12
Query Match: 21.45% Indels: 0
DB: 7 Gaps: 0

US-09-833-222A-10 (3-1090) x CO424223 (1-765)
Qy 395 LeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSerArgProMetVal 414
Db 1 CTGGCGGATGCGCAGGAGAGCGGTGAGTACTGCTGCTGTAGCCGCCCATGGTC 60
Qy 415 IleAsnHisAspHisAspIleIleThrGluAlaTyrMetAspSerLysLeuLeuSer 434
Db 61 ATCAACCATGACCAACGACATCATCTGGACAGAGGCTTACATGGACAGCGGCTCTTCACA 120
Qy 435 SerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProValPheSerLysLys 454
Db 121 TCAGAGGCGCAGAGCGCTGATGCTCTCCACACAGTGGCCATGCTGTCTTCAGCAAAAAG 180
Qy 455 AsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAspValAlaLeuArg 474
Db 181 AATGAAACAAGATCCCATGGCATTCCTCTGGGTGTAGTGGGCTCTGACGTGACCCTAAGA 240
Qy 475 GluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyrAlaPheLeuAsn 494
Db 241 GAGCTCATGAAGCTGGCACCCTCATATAAGCTTGGGGTGCATGGCTATGCTCTTCTGAAC 300
Qy 495 ThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyrArgGluGlyLys 514
Db 301 ACTAACATGGCTACATCTCTCTCATCTGACCTCGACCTTGTACAGAGAAGGCAAG 360
Qy 515 LysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluValGluTyrGluAsp 534
Db 361 AAGCTGAGACCCCAACCCCACTACAACAGTGTGGAGCTCTTCAGAAAGTGGAGTGGAGGAC 420
Qy 535 GlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThrLeuSerMetAsp 554
Db 421 CAAGCTGGAATTCCTGAGGACCGCCATGATCAATGGGGAAACCGGGTCTCTACTCCATGGAC 480
Qy 555 ValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsnAspTyrPhePhe 574
Db 481 GTGAAGGTGCCACTGGACAAAGGAAGCGAGTTCATTCTCTGACCAATGACTACTTCTTC 540
Qy 575 ThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArgGlyHisGlyGlu 594
Db 541 ACAGACATCAGTGCACACACCTTTTCAGCTGGGAGTGGTGTCTCACCAGAGGTTCATGGAGAA 600
Qy 595 TyrIleLeuGlyAsnThrSerValGluGlyLeuHisAspLeuLeuHisProAsp 614
Db 601 TACATCTCTCTGGGGAACACATCTGTGGAAAGAGGCGCTGCACGACTTGTCTCATCCGGAT 660
Qy 615 LeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspProAspHisArgLys 634
Db 661 CTGACCTTGGCCAGTGCCTGGATCTACTGTATACAGATATCCACCGGACCCCGGAAA 720
Qy 635 LeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAsp 649
Db 721 CTCAGCAACCTGGAAGCTGTGGTTCGTTTCCTGACAGGGGTGGAT 765

RESULT 12
BQ919363
LOCUS
DEFINITION AGENCOURT_8779072 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6373010
5', mRNA sequence.
ACCESSION BQ919363
VERSION BQ919363.1 GI:223334061
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```



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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 940)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabe-remail.nih.gov
Tissue Procurement: DCTD/DTF/Gazdar
cDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM2549 row: 1 column: 03
High quality sequence stop: 524.

FEATURES
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/clone="IMAGE:6373010"
/tissue_type="large cell carcinoma"
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/clone_lib="NIH_MGC_18"
/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 5.64e-120 Length: 940
Score: 1208.00 Matches: 236
Percent Similarity: 83.62% Conservative: 4
Best Local Similarity: 82.23% Mismatches: 13
Query Match: 21.10% Indels: 34
DB: 5 Gaps: 3

US-09-833-222A-10 (1-1090) x BQ919363 (1-940)

Qy 787 AlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArg 806
Db 19 GCCCGCGGCTCCAAATGAAGTGGATTCCTCCAGCGCAATTCCTGGCGGCAACGCG 78
Qy 807 GlnCysSerThrValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCys 826
Db 79 CAGTGCAGCAGCTGTGGATGGCGGTGCACACAGAGCTCCGAGGACAGTGTCTGGACTGC 138
Qy 827 PheValIleAspAanAnGlyPheIleSerLysArgSerArgGluThrGlyArg 846
Db 139 TTCGTCTACGACAAACAGGGTTCATTCGTATCTCCAGAGGTCCTCCGA----- 186
Qy 847 PheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuSerMetGlyValPheSer 866
Db 186 ----- 186
Qy 867 Gln-ValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisSerAl 886
Db 187 GAGAGTGACTATGATGACTATCAGGCGCATGTGCACACCCCTCGAGTCCACACACAGTGC 246
Qy 886 aAlaGlnProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuGlu 906
Db 247 AGCCACGCCCCCTGGTCAGCCCAATTCCTGCTCTTTCAGCGCGACCGAGGTGGCTGCA 306
Qy 906 nGluLeuValLeuPheLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAl 926
Db 307 GGAGCTGGTCTGTTCTCTGGAGTGGAGTGTCTGGGGCTCTCTGGTACGACAGAGGGGC 366

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Qy 926 aGluAlaLysSerValPheHisSerHisLysHisLysGlnAspProLeuGlnPr 946
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Db 427 CTGCGACACGAGTACCCCTGCTGTTGTTGTCACCGCGGCATCCGGGAGGCCAAGGAT 486
Qy 966 eValGluCysGlyProCysGlnLysValPheValValGlnIleProAsnSerAsnLe 986
Db 487 CGTGGAGTGGCGGCCCTCCAGGAAGTATTGTTGTCAGCAGATTCCTCAACAGTAACCT 546
Qy 986 uLeuLeuValThrAspProThrCysAspCysSerIlePheProProValLeuGlnI 1006
Db 547 CTTCTCTGTTGACAGACCCACCTGTGATGTGAGATCTTCCACCAAGTGTGCAAGGA 606
Qy 1006 uAlaThrGluValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLe 1026
Db 607 GCGACAGAAAGTCAATATATATGCTCTGTCAATGTGACCGGATGGCTCCAGAGACT 666
Qy 1026 uArgArgArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspAr 1046
Db 667 CCGCGCGCAGCAGACTCTCTGCCACGCTTCCATCCAGAGGAGAAATGCCCGGATGGCTCC 726
Qy 1046 g-GlyTrpAlaGly-----PheSerSerProAsnProLeuCysLeu----- 1059
Db 727 GCGCGCGCTCCGACACTCAGCCTCGCCGCCCTACTCTCTGGCTGGGNGGGGCGCC 786
Qy 1060 -----GlyLeuCysPro 1063
Db 787 TGGGGGGCTACTGCCCC 803

RESULT 13
BI908463
LOCUS
DEFINITION
603069223F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5218349 5',
mRNA sequence.
BI908463
VERSION
BI908463.1 GI:16171419
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
1 (bases 1 to 777)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabe-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LIAM11548 row: m column: 06
High quality sequence stop: 777.

FEATURES
Location/Qualifiers
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/clone_lib="NIH_MGC_118"
/notes="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range

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1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:			
Pred. No.:	2,43e-117	Length:	777
Score:	1182.50	Matches:	233
Percent Similarity:	85.92%	Conservative:	5
Best Local Similarity:	84.12%	Mismatches:	12
Query Match:	20.65%	Indels:	29
DB:	4	Gaps:	2

US-09-833-222A-10 (1-1090) x BI908463 (1-777)

Qy	789	GlyValGlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCys	808
Db	3	GGCGTCCAAATGAAGCTGGAAATTCCTCAGCGCAAAATTCGGCGGCAACGCGCAGTGC	62
Qy	809	SerThrValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheVal	828
Db	63	AGCACTGTGGATGGCGCGTGCACACAGAGTCCGAGGACAGTATCTGGACTGCTTCGTC	122
Qy	829	IleAspAsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeu	848
Db	123	ATCGACAACAACGGGTTTCATTCGTATCTCCAAGAGGTCCCGA	164
Qy	849	GlyGluValAspGlyAlaValLeuThrGlnLeuSerMetGlyValPheSerGln-Va	868
Db	165	-----GAGAGT	170
Qy	868	lThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisSerAlaAlaGln	888
Db	171	GACTATGTATGACTATCAGGCCATGTCAAAACCTCGAGTCACACACAGTGCAGGCCA	230
Qy	888	nProLeuValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuGlnGluLe	908
Db	231	GCCTCTGGTCAGGCCAATTTCTGCTTCTTTGACGGCAACAGGTGGCTGTCGAGGAGCT	290
Qy	908	uValLeuPheLeuLeuGluTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAl	928
Db	291	GGTGTCTTCTCTGGAGTGGAGTGTCTGGGCTCTGTGTACGACAGAGGCGCGAGGC	350
Qy	928	aLysSerValPheHisSerHisLysHisLysLysGlnAspProLeuGlnProCysAs	948
Db	351	CAAAAGTGTCTTCATCACTCCCAACAAACACAGACAGACCCGCTGCAGCCCTCGGA	410
Qy	948	pThrGluTyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValG1	968
Db	411	CACGGAGTACCCCGTGTCTGTACACCGCGGCATCCGGAGGCGCAACGGATCGTGA	470
Qy	968	uCysGlyProCysGlnLysValPheValGlnGlnIleProAsnSerAsnLeuLeuLe	988
Db	471	GTGCGGCGCTTCGAGAGGATATTGTGGTGGCAGAGATCCCAACAGTAACCTCTCTCT	530
Qy	988	uLeuValThrAspProThrCysAspCysSerIlePheProValLeuGlnGluAlaTh	1008
Db	531	CTGTGTGACAGAGCCCACTGTGCTGCACATCTTCCACACAGTGTGCAGAGGCGGAC	590
Qy	1008	rGluValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgAr	1028
Db	591	AGAAGTCAAAATATAATGCCTCTGTCAATGTGACCGGATCGCTCCCAAGATCCGCGC	650
Qy	1028	qArgProAspSerCysHisAlaPheHisProGluValArgValGluAlaAspArgGlyTr	1048
Db	651	GCAGCAGAGTCTCTGGCACCGCTTCCATCCAGAGGA-CGAATGCC-CAGGACTCGCGCG	708
Qy	1048	pAlaGlyPheSerSerProAsnPro-----LeuCysLeuGlyLeuCys 1062	
Db	709	CGCTCGGACAGCTCAGCCTCGCGCCCTTACTTCTTCTGCTGCTGTGTGT 757	

AK044603
LOCUS
DEFINITION

AK044603 3527 bp mRNA linear HTC 03-APR-2004
Mus musculus adult retina cDNA, RIKEN full-length enriched library,
clone:AF90026F23 product:calcium channel, voltage-dependent, alpha
2/delta subunit 2, full insert sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AK044603.1 GI:26336630
HTC; CAP trapper.
Mus musculus (house mouse)

REFERENCE

1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2
REFERENCE

AUTHORS

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
3
REFERENCE

AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Iehi, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohata, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4
REFERENCE

AUTHORS

The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
REFERENCE

AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3527)
REFERENCE

AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Inotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Oheato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akaira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission

TITLE

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Retina RNA was provided by Dr. Stefano Gustigich (Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA 02115, USA) whose assistance is gratefully acknowledged. Please visit our web site for further details.
URL: <http://genome.gsc.riken.jp/>
URL: <http://fantom.gsc.riken.jp/>
Location/Qualifiers

FEATURES

source

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CDS

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ORIGIN

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Alignment Scores:
Pred. No.: 6,04e-116 Length: 3527
Score: 1180.00 Matches: 345
Percent Similarity: 47.77% Conservative: 202
Best Local Similarity: 30.13% Mismatches: 426
Query Match: 20.61% Indels: 172
DB: 3 Gaps: 44

US-09-833-222a-10 (1-1090) x AK044603 (1-3527)

Qy 16 TrpAlaAspThrPheGlyGlyAspLeuTyraAsnThrValThrLysTyrsrGlySerLeu 35
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Qy 56 LeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeuArgArgLysValGlu 75
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Qy 96 SerLeuValPheAsp-----TyrTyraAsnSerValLeuLysLeuAsnGluArgAsp--- 111
Db 471 AACATCAAGGAGGAGACATCATGTACTAGCTCAAGGCTGACGCGGCTGATGATGAC 530
Qy 112 -----GluLysGlyAsnPheValGlu---LeuGlyAlaGluPheLeu 124
Db 531 CCTGAGAGTGAAGATATGGAGAGGGGATCCAGACACGAGCGCTTAAGGCTGGACTTCATC 590
Qy 125 LeuGluSerAsnAlaHisPheSerAsnLeuProValAsnThrSerIleSerSerValGln 144
Db 591 GAGGACCCAAAC-----TTCAAGAAC---AAAGTCAACTATTTCATACACGCGTGTGCAG 641
Qy 145 LeuProThrAsnValTyraAsnLysAspProAspIleLeuAsnGlyValTyMetSerGlu 164
Db 642 ATCCCCACACACATCTTACAAGGCTCTACCGCTCATCTCAATGAGCTTTAACTGGACAGAG 701
Qy 165 AlaLeuAsnAlaValPheValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyr 184
Db 702 GCCTTGGAGAACGCTCTTCAATTGAGAACCGTAGGACAGACCTTACACTGTTGTGGCAAGTC 761
Qy 185 PheGlySerAlaThrGlyPhePheArgIleTyrProGlyIleLysTrpThrProAspGlu 204
Db 762 TTTGGCAGTCCACGGGAGTCACTCGCTATTATCCAGCCACACCATCGCAGGCCCCAAG 821
Qy 205 AsnGlyValIleThrPheAspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSer 224
Db 822 AAG---ATTGACCTGTACGATGTCAAGAACGACCCCTGGTATATACAGGGGCGCTCATCA 878
Qy 225 ProLysAspIleValIleLeuValAspValSerGlySerMetLysGlyLeuArgMetThr 244
Db 879 CCCAAGACATGTTCATATTGTTGGATGTGAGTGGGAGCGTGAGCGGCGCTGACTCTGAAG 938
Qy 245 IleAlaLysHisThrIleThrIleLeuAspThrIleLeuGlyGluAsnAspPheValAsn 264
Db 939 CTGATGAAGACGTCGCTCTGTGAGATGCTAGACACGCTCTCTGATGATGATATGTGAAC 998
Qy 265 IleIleAlaLysAsnAspTyrValHisTyrIleGluProCysPheLysGlyIleLeuVal 284
Db 999 GTGGCTTCATTCAACAGGAGGCGGCGCTGTGTCT---TGCTTCACACAC---CTGTGTG 1052
Qy 285 GlnAlaAspArgAsnArgGluHisPheLysLeuLeuValGluGluLeuMetValLys 304
Db 1053 CAGGCCAATGTGCGTAACAAGAGGTGTTCAAGGAGCTGTGCAGGCGCATGGTGGCCAG 1112
Qy 305 GlyValGlyValValAspGlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGln 324
Db 1113 GGCACACACAGGCTACAAGGCGGCTTTGAGTATGCTCTTTCACAGCATACAGAATTCACAC 1172
Qy 325 GluAlaLysGlnGlySerLeuCysAsnGlnAlaIleMetLeuLysSerAspGlyValAla 344
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Qy 345 GluAspTyrGluProValPheGluLysTyrAsnTrpProAspCysLysValArgValPhe 364
Db 1227 GATCGCGTGCAGGATGCTCTTCCGAAGAAGTACAATTGGCCCAATCGGACGGTACGCTGTC 1286
Qy 365 ThrTyrLeuIleGlyArgGluValSerPheAlaAspArgMetLysTrpIleAlaCysAsn 384
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Qy 385 AsnLysGlyTyrThrThrGlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGlu 404
Db 1347 AACAAAGGTACTATTTTGAGATCCCTTCCATCGGAGCCATCCGATCAACACACAGAA 1406
Qy 405 TyrLeuHisValLeuSerArgProMetValIle-----AsnHisAspHisAspIle 422
Db 1407 TACCTGGATGTGCTGGTAGGCCCATGTTACTGGCAGGCAAGGACGCGCAAGTGCACAA 1466
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Db	3408	CCGCAGCCTCAAGTC	3422	
RESULT 15				
LOCUS	BG436760			
DEFINITION	60248181P1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4620980 5',	725 bp	mRNA	linear EST 14-MAR-2001
ACCESSION	BG436760			
VERSION	BG436760.1	GI:13343177		
KEYWORDS	EST.			
SOURCE	Homo sapiens			
ORGANISM	Homo sapiens (human)			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .			
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)			
COMMENT	Unpublished (1999)			
	Contact: Robert Strausberg, Ph.D.			
	Email: cgapbs-remail.nih.gov			
	Tissue Procurement: DCTD/DTF/Gazdar			
	cDNA Library Preparation: Ling Hong/Rubin Laboratory			
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			
	DNA Sequencing by: Incyte Genomics, Inc.			
	Clone distribution: MGC clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LLNL at:			
	http://image.llnl.gov			
	Plate: LLC1383 row: b column: 21			
	High quality sequence stop: 723.			
FEATURES	Location/Qualifiers			
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	/organism="Homo sapiens"			
	/mol_type="mRNA"			
	/db_xref="taxon:9606"			
	/clone="IMAGE:4620980"			
	/tissue_type="large cell carcinoma"			
	/lab_host="DH10B (phage-resistant)"			
	/clone_lib="NIH_MGC_18"			
	/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:			
	EcoRI; cDNA made by oligo-dT priming. Directionally cloned			
	into EcoRI/XhoI sites using the following 5' adaptor:			
	GGCAGCAG(G). Library constructed by Ling Hong in the			
	laboratory of Gerald M. Rubin (University of California,			
	Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and			
	Superscript II RT (Life Technologies). Note: this is a			
	NIH_MGC Library."			
ORIGIN				
Alignment Scores:				
Pred. NO.:	1.14e-114	Length:	725	
Score:	1157.50	Matches:	225	
Percent Similarity:	88.98%	Conservative:	1	
Best Local Similarity:	88.58%	Mismatches:	3	
Query Match:	20.21%	Indels:	27	
DB:	4	Gaps:	1	
US-09-833-222A-10 (1-1090) x BG436760 (1-725)				
Qy	787	AlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLysPheTyrAlaAlaThrArg	806	
Db	38	GGCCGGGGCGTCCAAATGAAGCTGGAATTCCTCAGCGCAAAATTCCTGGGGGCAACGGG	97	
Qy	807	GlnCysSerThrValAspGlyProTyr*ThrGlnSerCysGluAspSerAspLeuAspCys	826	
Db	98	CAGTGCAGCACTGTGGATGGCCCTGCACAGAGCTGCGAGGACAGTGTGGAATGC	157	
Qy	827	PheValIleAspAsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArg	846	
Db	158	TTTCGTATCGACAACAACGGGTTCATTCTGATCTCCAAGAGGTCCCGA-----	205	
Qy	847	PheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSer	866	
Db	205	-----	205	

Search completed: November 17, 2005, 05:33:34
Job time : 8110 secs

Qy	867	Gln-ValThrMetTyrAspTyrGlnAlaMetCysLysProSerSerHisHisSerAl	886
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Db	266	AGCCACGCCCTGGTCAGCCCAATTTCTGCTTCTTGACGGCGACAGTGGCTGTGCA	325
Qy	906	nGluLeuValLeuPheLeuLeuGluTTPSerValTTPGlySerTTPtyrAspArgGlyAl	926
Db	326	GGAGCTGGTCTGTCTCTCTGGAGTGGAGTGTCTGGGGCTCTCTGGTACGACAGAGGGC	385
Qy	926	aGluAlaLysSerValPheHisSerHisLysHisLysLysGlnAspProLeuGlnPr	946
Db	386	CGAGGCCAAAAGTGTCTTCCATCATTCCCAACACCAAGAGCAGGCCCTGCAGCC	445
Qy	946	oCysAspThrGluTyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyI1	966
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Qy	966	eValGluCysGlyProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLe	986
Db	506	CGTGGAGTGGGGCCCTGCCAGAGGTATTTGTGTGCAGCAGATTCCCAACAGTAACCT	565
Qy	986	uLeuLeuLeuValThrAspProThrCysAspCysSerIlePheProProValLeuGlnG1	1006
Db	566	CCTCTCTGGTGACAGACCCACCTGTGACTGTGAGCTGCAGCATCTTCCACACAGTGTGCAGGA	625
Qy	1006	uAlaThrGluValLysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLe	1026
Db	626	GGCGACAGAAAGTCAATATATATGCTCTGTCAATGTGACCGGATGCGCTCCCAAGAGCT	685
Qy	1026	uArgArgArgProAspSerCysHisAlaPheHisProGlu	1039
Db	686	CCG-CGGCGACA-GACTCTCTGCCACGGCTTCCATCCAGAG	723

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 03:13:48 ; Search time 49 Seconds
(without alignments)
2140.332 Million cell updates/sec

Title: US-09-833-222a-10
Perfect score: 5726
Sequence: 1 MAVALGTRRRDRVKLWADTF.....MPMNTVPVVLGGNIRVYAL 1090

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3422	59.8	1091	2 T30256	calcium channel al
2	1089	19.0	1106	1 CHRB2	calcium channel pr
3	1077.5	18.8	1091	2 JH0565	calcium channel al
4	1056.5	18.5	1091	2 A44147	calcium channel pr
5	638.5	11.2	734	2 S44617	CSOC3.11 protein -
6	543	9.5	1148	2 T18770	probable calcium c
7	209.5	3.7	1450	2 C86880	hypothetical prote
8	175	3.1	946	1 IYHU2	inter-alpha-trypsi
9	172.5	3.0	946	2 JC5575	inter-alpha-trypsi
10	166.5	2.9	946	2 S54354	inter-alpha-inhibi
11	164.5	2.9	930	2 JX0368	inter-alpha-trypsi
12	150.5	2.6	889	2 JC5576	inter-alpha-trypsi
13	148.5	2.6	886	2 S54355	inter-alpha-trypsi
14	146.5	2.6	885	2 S30350	inter-alpha-trypsi
15	145.5	2.5	2819	2 A90551	conserved hypotet
16	144.5	2.5	921	2 JC4625	inter-alpha-trypsi
17	144	2.5	820	2 AD2357	hypothetical prote
18	144	2.5	1091	2 C95133	exonuclease REXB I
19	144	2.5	1091	2 G98001	second chain of ma
20	143	2.5	655	2 S59836	hypothetical prote
21	142	2.5	911	2 A39867	inter-alpha-trypsi
22	140.5	2.5	570	2 AC2356	hypothetical prote
23	135.5	2.4	676	2 T47637	hypothetical prote
24	135	2.4	436	2 E90261	hypothetical prote
25	134.5	2.3	1276	2 S11455	botulinum neurotox
26	134.5	2.3	1329	2 AE1901	WD-repeat containi
27	134	2.3	1073	2 S14032	kinesin-related pr
28	132.5	2.3	918	2 E90542	lipoprotein [impor
29	131.5	2.3	2280	2 T38906	acetyl-CoA carboxy

30 131 2.3 1085 2 T38378
31 129.5 2.3 587 2 I64023
32 129.5 2.3 906 2 D82899
33 129.5 2.3 1188 2 F64367
34 129 2.3 802 2 C90326
35 129 2.3 932 2 JC5953
36 129 2.3 8243 2 T31307
37 128 2.2 689 2 F84811
38 128 2.2 914 2 JC5574
39 127.5 2.2 709 2 AD2843
40 127.5 2.2 717 2 E97620
41 127 2.2 629 2 C83107
42 126.5 2.2 1411 2 S55123
43 126.5 2.2 2279 2 T42531
44 124.5 2.2 885 2 AB1944
45 123.5 2.2 2670 2 T37919

ALIGNMENTS

RESULT 1

T30256

calcium channel alpha-2-delta-C chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

C:Accession: T30256

R:Klugbauer, N.; Lacinova, L.; Marais, E.; Hobom, M.; Hofmann, F.

J. Neurosci. 19, 648-691, 1999

A:Title: Molecular diversity of the calcium channel alpha2delta subunit.

A:Reference number: Z20794

A:Accession: T30256

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1091 <KLU>

A:Cross-references: UNIPROT:Q9Z1L5; EMBL:AJ010949; PIDN:CAA09423.1

A:Experimental source: brain

C:Superfamily: calcium channel alpha-2 chain

Query Match 59.8%; Score 3422; DB 2; Length 1091;
Best Local Similarity 60.0%; Pred. No. 1.5e-217;
Matches 627; Conservative 188; Mismatches 212; Indels 18; Gaps 6;

Qy	13	VKLWADTFGGDLNTVNTKYSGSLLQLKKYKDVSSLLKIEVDGLLELRKSEDMENLMRR	72
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Qy	73	KVEAVQNLVEAEEADLNHEFNSLVFDYVNSVLINERDEKGNFVEIGAEFLLESNAHFS	132
Db	102	KSEAVRRLVEAEEAHLKHEFDADLQYEFNAVLINERDKGNFLEIGKGFILAPNDHFN	161
Qy	133	NLPVNTSISVQLPTVNTYKNDPDLNGVYVNSEALNAVVFENFORDPTLTWQYFGSATGFF	192
Db	162	NLPVNTSLSDVQVPTNMYNKDPAIVNGVYVNSEALNAVVFENFORDPTLTWQYFGSATGFF	221
Qy	193	RIYPGIKWTPDENGVTFFDCNRNGWIQAATSPKDVILVDVSGSMKGLRMTIAKHITT	252
Db	222	QYPGIKWEPDENGVIATFDCNRNRKWIQAATSPKDVILVDVSGSMKGLRTIAKQTVSS	281
Qy	253	ILDTLGDNDPVNLIANDVYHYIEPCFKGLVQADRDNRHEFKLLVLEELVKGVVQDOA	312
Db	282	ILDTLGDNDPFNITTYNEELHYEPCFKGLVQADRDNRHEFKLLVLEELVKGVVQDOA	341
Qy	313	LREAFQILKQFQBAKQSLCNQAIMLISDGAVDYEPVFEKYNWPCDKRVVFTYLIQREV	372
Db	342	LNEAFNLSDFNTGTGQSICQAIMLITDGAVDYDTIFAKYNWPCDKRVVFTYLIQREV	401
Qy	373	SPADRMKVIACNNKGYTYTISTLADQENVMYHLVSRPMVINHDHDIITWEAYMOSKL	432
Db	402	AFADNLKWMACANKGFTFTISTLADQENVMYHLVSRPMVINHDHDIITWEAYMOSKL	461
Qy	433	LSSQA----QSLTLLTTPVAMPVSKNETSHGILLGLGVSDVALRELMLKAPRYLGVH	488

Db 462 POAQLADDOGLVMTTVAAMPVFSQKQNETRSGKILLGVGVTDPVKELTKTIPIKYKLGIIH 521

Qy 489 GYAFINTNNGYILSHPDRLPLRYEGKKPKKPNTNSVDLSSEWEDQAESLRTAMINRET 548

Db 522 GYAFINTNNGYILSHPDRLPLRYEGKK-RRKPNYSVDLSSEWEDRDDVLRNANVRKT 580

Qy 549 GTLSMDVKVPMQKGRVLFITNDYFTDIIDTPFSLGAVLSRGHGEYILLGNSTSVESGLH 608

Db 581 GKFSMEVKTKVDKGRVLMVNTDYYTDIKGTPFSLGVALSRGHGKYFFRGVNTIEBGLH 640

Qy 609 DLLHPDLALAGDWIYCTIDDPDRKLSQLEAMIRFTRKDPDLCEBELVREVLDAVV 668

Db 641 DLEHPDVLADSESYCNLDLHPEHLSQLEAIKLYLKGKEPLQCDKELIQEVLDAVV 700

Qy 669 TAPMEAYTALALNMSSEHVDMAFLGTRAGLLRSSLFVSGEKVSDRKLTPDEASV 728

Db 701 SAPIEAWTSLALNKSNSDKGEVAFGLGTRGLSLRNLFVGAELTNQDFLKGADKENI 760

Qy 729 FTLDLRFPLWYQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVATVDKRTAIAAAA 788

Db 761 FNADHFLWYRRAAEQIAGSFVYSIPSTG-TVKNVNVVTAFTSIQLLDERKSPVVAAV 818

Qy 789 GVQMKLEFLQKFWAATROGSTVDGPTQSCEDSDLCFVIDNNGFLLISKRRETRGFL 848

Db 819 GIOMKLEFFQKFWATROQASLDGKCSISCDDETVCYLIDNNGFLLVSEDTYQTGDF 878

Qy 849 GEVDGAVLTOLLSMGVFSQVMTDYQAMCKPSSHHSAAQPLVSPISAFLTATRWLLOEL 908

Db 879 GEVEGAVMKNLLTWGSEFKRITLDYQAMCRANKESSDSANGLDLPYKAFLSAAKNWTEL 938

Qy 909 VLFELLESVMGWSYDGAEAASVPHSHHGKQDPQPCDTEYFVYQPAIREANGIVE 968

Db 939 VLFELVEFNLCS-SNWSHDMTAKA-----QKLEKQTEPCDTEYPAFVSERTIKETTGNIA 990

Qy 969 CGPCQKVFVVOQTPNSNLLLVLTDPDTCDSIFPPVQLEATEVKNASVKCDMRSKLRR 1028

Db 991 CEDCSKSFVQIQPSSNLFVWVVDSSCLCESVAPITMAPIEIRYNESLKCERLKAQKIRR 1050

Qy 1029 RPDSCFAPHPVEVRVADRGWAGFSS 1053

Db 1051 RPESCHGFPE---ENARECGGASS 1072

RESULT 2

CHRB2

calcium channel protein alpha-2 chain precursor - rabbit

N;Alternate names: dihydropyridine-binding protein, 140K

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text_change 09-Jul-2004

C;Accession: S10579; A39518; A33409

R;Ellis, S.B.; Williams, M.E.; Ways, N.R.; Brenner, R.; Sharp, A.H.; Leung, A.T.; Campbell, S.C. 1988

A;Title: Sequence and expression of mRNA encoding the alpha(1) and alpha(2) subunits of the dihydropyridine-sensitive calcium channel

A;Reference number: S10579; MUID:88336904; PMID:2458626

A;Accession: S10579

A;Molecule type: mRNA

A;Residues: 1-1106 <ELL>

A;Cross-references: UNIPROT:P13806; EMBL:M21948; NID:g164762; PIDN:AAA81562.1; PID:g1647

A;Note: 57-Asp, 106-Lys, and deletion of 620-Ser were also found

R;Jay, S.D.; Sharp, A.H.; Kahn, S.D.; Vedvick, T.S.; Harpold, M.M.; Campbell, K.P. J. Biol. Chem. 266, 3287-3293, 1991

A;Title: Structural characterization of the dihydropyridine-sensitive calcium channel

A;Reference number: A39518; MUID:91131638; PMID:1847144

A;Accession: A39518

A;Molecule type: protein

A;Residues: 361-973 <JAY>

A;Note: this sequence represents the amino end of a glycosylated peptide that appears at the amino end and identical molecular weights (17K) following deglycosylation

R;Hamilton, S.L.; Hawkes, M.J.; Brush, K.; Cook, R. Biochemistry 28, 7820-7828, 1989

A;Title: Subunit composition of the purified dihydropyridine binding protein from skeletal muscle

A;Reference number: A33409; MUID:90122765; PMID:2558713

A;Accession: A33409

A;Status: preliminary

A;Molecule type: protein

A;Residues: 27-44, 'S', 46-47 <HAM>

C;Superfamily: calcium channel alpha-2 chain

C;Keywords: calcium; disulfide bond; glycoprotein; ion channel; membrane protein; phosphatase

F;1-26/Domain: signal sequence #status predicted <SIG>

F;27-1106/Product: calcium channel alpha-2 chain #status predicted <MAT>

F;94,138,186,326,350,470,477,606,615,678,697,784,827,891,898,988,1001,1081/Binding site:

Query Match 19.0%; Score 1089; DB 1; Length 1106;

Best Local Similarity 28.0%; Pred. No. 26-63;

Matches 315; Conservative 222; Mismatches 431; Indels 156; Gaps 44;

Qy 13 VKLWADTFGDLVNTVTYKSGSLLLQKKYKDVSSLLKIBEVDSGLVLRKFSDEMNLRR 72

Db 35 IKSWDKMQEDLVTLAKTAGVGHQVLDIYEKYQDLTYVEPNARQLVETIARDIEKLLSN 94

Qy 73 KVEAVQNLVEAAEADLNHEFNESLVD---YNSVLINERDEKGNFVELGAE-----FL 124

Db 95 RSKALVRLALEAEKVQAAHQWREDFASNEWVYNAK--DDLDPKNDSEBGSQRIKPVFI 152

Qy 125 LSNHAFSLPNTSSVQLPTNVYKDPDILNGVYMSALNAVFNFPQDPTLTWQY 184

Db 153 DDAN---FRQVSYQHAHVHIPTDIYEGSTIVLNELNWTLSALDDVFKQREEDPSLLQV 209

Qy 185 FGSATGFFRIYPGIKWTPDE---NGVITFCRNRGWYIQAAQSPKDIKIVLDVDSGSMKGL 241

Db 210 FGSATGLARYYPASPMVDSNRTPNKIDLDVRRRPWYIQGAASPKDMLILVDVSGVSG 269

Qy 242 RMTAKHTITLDTLGENDFVNIYAYNDVHYIIEPCFKGILVQADRDNRHFKLIVLEEL 301

Db 270 TLKLRTSVSEMLETLSDDDFNVASFNSAQDVS-CFQH-LVQAVNRKKVLKDAVNI 327

Qy 302 MKGVGVVDQALREAFQILKQEAQKQSLCQAIIMLSGDAVEDYEPFEKYNWDCVK 361

Db 328 TAGKITDYKGFSAPEQLNLYNVSRAN--CNKIIMLFTDGGEEAQAEIFAKYN-KDKKV 384

Qy 362 RVFTYILIGREVSFADRMKWIACNNKGYTQISTLADTQENVMYELHVLGRPMVNH--H 419

Db 385 RVFTSVGQHYDRGPIQWACENKGYEIEISGAIRINTQEIYLDVLRGPMVLADGKAK 444

Qy 420 DIITEAYNDSKLLSSQAQSLTLTTVAMPVFS---KNETR-SHGILLGVVGSVAUR 474

Db 445 QVQWNTNVYLD-----ALELGLVITGTLPVFNITQGFENKTNLKNQLILGVMGVDVSL 497

Qy 475 ELMKLAPRYKLVGHGYAFLNTNNGYILSHPDRLPLYRECKL-----KPKNYN- 523

Db 498 DIKRLTPRFLPCNGYFAIDPNGYVLLHPNIDP-----KPIGVGIPITNLKRRRPNVQN 552

Qy 524 -----SVDLSEVEWEDQAE-SLRATMINRETGTLSMDVKVP-----MDKGRVLF 569

Db 553 PKSQEPVTLDFDLDAELENDIKVEIRNKMIDGESGEKFTLVKSQDERYIDKGNRT---- 608

Qy 570 NDYFTDISDTPFSLGAVLSRGHGEYIL---LGNTSVSEGLHDLHPD-----LALAG 620

Db 609 --YTWTVPNGTDYSSIALVLPTYSFYIKAKIETITQARYSETLKPDPFESGYTFLAP 666

Qy 621 WYCYCTIDDPDRKLSQLEAMIRFTRKDP-DLECDLAVREVLDAVTPM-EAYWTA 678

Db 667 RQYC-SDLKPSDNNTFLLNFNEFIDRKTTPNPSNCTDLINRVLLDAGFTNELVQWYS- 724

Qy 679 LALNMSSEHVVVDMAFLGTRAGLLRSSLFVSGEKVSDRKLTPDEASVFTLDRPPLWY 738

Db 725 -----KQNKIKGVKARFVVTDGDIR---VYPKEAGENWQENPEYEDSF-----Y 767

Qy 739 ROASEHPAGSFVFNLRW---AEGPESAGEPMVVTASTAVATVDVKRTAIAAAGVQMKLF 796

Db 768 KRLSN--DNYVFTAPYFNKSGFGAYESGIMV--SKAVEIYIQGKLLKPAVGIKIDVNS 823

Qy 797 LQKFWAATRO--CSTVDGPTQSCEDSD-LDCFVIDNNGFLLISKR---SRETGRFLGR 850

Db 824 WIENFTKTSIRDPCA---GPVCCDKNSDVMOCVILDDGCGFLMANHDDYTIQIGRFFGE 880

Qy 851 VDGAVALTQLSMGVFSQVMTYDQAMCKP-----SSHHSAAQPLVS-----PISAFLTAT 901
 Db 881 IDPSLMRLHVNISYAFNKSVDYQSVCEPAAKQAGHRSAYVPSIADILQIGWATAA 940
 Qy 902 RW-LLOELAVLFLLEWSVMGSDYDGAAGAKSVFHHSHKHKKODPL-----QPCDTEYPVF 954
 Db 941 AWSILQQFLSLT-----FPLLEAADN-----EDDDFTASMSKQSCITEQTQY 984
 Qy 955 VYQPAIREANGIVEGCPQKVFVVQQIPNSNLLLLVTD--TCDCSIFPPVLOBAATEVKY 1012
 Db 985 FFDNDSKFSVGLDGCNCSRIHFVEKLMNTNLIIFIMVESKGTCTCDTRLIIQAQOTS--- 1041
 Qy 1013 NASVKCDRMSQKLRRRDPDSCHAFHPEVRVADRGWAGFSSPNP 1056
 Db 1042 DGPDPCDMVKQPRYKGPDVC--FDNNV-LDYTDCGVSGLNP 1082

RESULT 3
 JH0565
 calcium channel alpha-2b chain precursor - human
 C;Species: Homo sapiens (man)
 C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C;Accession: JH0565
 R;Williams, M.E.; Feldman, D.H.; McCue, A.F.; Brenner, R.; Velicelebi, G.; Ellis, S.B.;
 Neuron 8, 71-84, 1992
 A;Title: Structure and functional expression of alphas, alpha2, and beta subunits of a r
 A;Reference number: JH0564; MUID:92110010; PMID:1309651
 A;Accession: JH0565
 A;Molecule type: mRNA
 A;Residues: 1-1091 <WLT>
 A;Cross-references: UNIPROT:P54289; GB:M76559; NID:g179761; PIDN:AAA51903.1; PID:g179762
 A;Experimental source: basal ganglia
 A;Note: Several conflicts are found between GenBank submission, authors' translation in
 C;Comment: This protein is a subunit of the voltage dependent calcium channel.
 C;Superfamily: calcium channel alpha-2 chain
 C;Keywords: glycoprotein; phosphoprotein
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-1067/Product: calcium channel alpha-2b chain #status predicted <CAL>
 F;32,268,326,539,635,1087/Binding site: phosphate (Thr) (covalent) (by protein kinase C)
 F;91,142,250,625,817/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #sta
 F;92,136,184,324,348,468,475,585,594,663,682,769,812,876,883,973,986/Binding site: carbo
 F;501/Binding site: phosphate (Thr) (covalent) #status predicted
 F;833/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predic

Query Match 18.8%; Score 1077.5; DB 2; Length 1091;
 Best Local Similarity 28.3%; Pred. No. 1.1e-62;
 Matches 315; Conservative 217; Mismatches 432; Indels 151; Gaps 44;

Qy 13 VKLMADTFGGDLVNTVTKYSGSLLLQKKYKDVESLKIIEVDGLLELVKFSDEMNMMLRR 72
 Db 33 IKSVVDKMQEDLVTLAKTAGVNLVDIYEKYQDLTYVEPNNAQLVEIAARDIEKLLSN 92
 Qy 73 KVEAVQNLVEAAEADLNHEFNESLVPD---YNSVLINERDEKGNFVGLAE-----FL 124
 Db 93 RSKALVSLALEAEKQAAQHOMREDFASNEVVYNAK--DOLDPEKNSEPGSQRIKPVFI 150
 Qy 125 LESNAHFSNLPVNTSISVOLPTVYVYKNDPDLNGVYMSALNAVVFENFQDPTLTWQY 184
 Db 151 EDAN---FGRQISVQHAHVIPDTDIYEGSTIVLNELNWTLSALDEVFKKNEEDPSLLMQV 207
 Qy 185 FGSATGFRFYPGIKWTPTDE---NGVITFCRNGWTYQIATSPKDIIVLDVSGSMKGL 241
 Db 208 FGSATGLARYYPASPVDNRSRTPNKIDLYDVRPRPWTYIQGAASPKDMLILVDVSGSVSGL 267
 Qy 242 RMTAKHTITITLDTLGENDPVNIAYNDVYHYTEPCFKGILVQADRDRNREHFLLVEEL 301
 Db 268 TLKIRTSVSEMLTSLDSDFPVNVASFNSNAQDVS-CFQH-LVQAVNVNKKVLKDAVNNI 325
 Qy 302 MVKGGVGVQALREAFQILKQFQBAQKQSLCNQAIMLISDGAVDYDFEYFVKYNWPDCKV 361
 Db 326 TAKGITDYKKGFSFAFQOLLNYSVRAN--CNKIIMLFTDGGEEAQAEIFNKYN-KDKKV 382
 Qy 362 RVFTYTLIGREVSFADRMKWIACNNKGYTQISTLADTQENVMYELHVLSPMVINHID--H 419

Db 383 RVFRFSVQGHNYRGPQIOMACENKGYEIPSGAIRINTQEQYLDLGRPMVLGAKAK 442
 Qy 420 DIITWEAYMDSKLLSSQAQSLTLLTTVAMPVFS-----KQNETR--SHGILLGVGSDVALR 474
 Db 443 QVQWTVYLD-----ALEGLVITGTLFVFNITGQFENKTNLKNQILLGVMGVDVSL 495
 Qy 475 ELMKLAPRYKLVGHVAFNLNTNGYILSHPDLPRLPYREGKKLKPKNVNSVDLSEVWEED 534
 Db 496 DIKRLTPRFTLCPNGYFAIDPNGYVLLHPNLPQ--KNPKSQEPV---TLDFLDLAELN 549
 Qy 535 QAB-SLRATMINRETGLSMDVKVP-----MDKGEVLFTINDYFPTDTSIDTSPFSLGAV 587
 Db 550 DIKVEIRNKMIDGESGEKTPRTLIVKSDERYIDKGNRT-----YTPVNGTDTISLALV 603
 Qy 588 LSRGHGEYILLGNTSVBEGL-----HDLHPD-----LALAGDWIYCIITDID 629
 Db 604 LPTYSFYI---KAKLEETITQARKSKGKMKDSETLKPDPNFESGYTFIAPRDYC-NDLK 659
 Qy 630 PDHRKLSQLEAMIRFLTRKOP-DLEDEELVREVLFDVAVTAPM-EAYWTALALNMSEES 687
 Db 660 ISDNTEFFLNFNEFIDRKTNNPNCNADLINRVLLDAGFTNELVQNYWS-----KQKN 713
 Qy 688 EHVVDMAFGLTRAGLLRSSLFVGSEKVSDDRKFLLTPPEDEASVFTLDRFPLWYROASEHPAG 747
 Db 714 IKGVKARFVVTDDGITR---VYPKEAGENWQENPETYEDSF-----YKRSLDN--D 759
 Qy 748 SFVFNLRW--AEPGESAGEPMVVTASTAVAVTVTKRTAIAAAGVQMKLEFLQKFWAAT 805
 Db 760 NYVFTAPYFNKSGPAGYESGMV--SKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTS 817
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 Db 818 IRDPACA---GPVDCCKRNSDVMCDVILDDCGFLMANHDDYTNQIGRFFGEBIDPSLMRHL 874
 Qy 860 LSNMGVFSQVMTYDQAMCKP-----SSHHSAAQPLVS---PISAFLTATRW-LLOELV 909
 Db 875 VNLISVAFNKSVDYQSVCEPAAKQAGHRSAYVPSIADILQIGWATAAAMSILOQFL 934
 Qy 910 LFLLEWSVMGSDYDGAAGAKSVFHHSHKHKKQDPL-----QPCDTEYPVVYQPAIREA 963
 Db 935 LSLT-----FPLLEAVEM-----EDDDFTASLSKQSCITEQTQYFPDNDKSF 978
 Qy 964 NGIVEGCPQKVFVQIQIPNSNLLLVTD--TCDCSIFPPVLOBAATEVKYNAVKSCDRM 1021
 Db 979 SGVLDCGNCRIHFGEKLMNTNLIIFIMVESKGTCTCDTRLIIQAQETSQDGN---PCDMV 1035
 Qy 1022 RSQKLRRRDPDSCHAFHPEVRVADRGWAGFSSPNP 1056
 Db 1036 KQPRYKGPDVC--FDNNV-LDYTDCGVSGLNP 1067

RESULT 4
 A44147
 calcium channel protein alpha-2 chain precursor - rat
 N;Alternate names: dihydropyridine-sensitive L-type
 N;Contains: calcium channel alpha-2 chain
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
 C;Accession: A44147
 R;Kim, H.L.; Kim, H.; Lee, P.; King, R.G.; Chin, H.
 Proc. Natl. Acad. Sci. U.S.A. 89, 3251-3255, 1992
 A;Title: Rat brain expresses an alternatively spliced form of the dihydropyridine-sensit
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 A;Accession: A44147
 A;Status: preliminary
 A;Molecule type: mRNA
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 A;Cross-references: UNIPROT:P54290; GB:M86621; NID:g203954; PIDN:AAA41088.1; PID:g203955
 C;Superfamily: calcium channel alpha-2 chain
 C;Keywords: calcium; glycoprotein; ion channel; transmembrane protein

Query Match 18.5%; Score 1056.5; DB 2; Length 1091;


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Qy 575 TDSDTPFSLGAVLSRG 591
Db 658 ECINHANFVLGLAVAKG 674

RESULT 6
T18770
probable calcium channel protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18770; T25249
R:Sulston, J.
submitted to the EMBL Data Library, June 1995
A:Reference number: Z19019
A:Accession: T18770
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1148 <W1>
A:Cross-references: UNIPROT:Q17517; EMBL:Z49907; PIDN:CAA90091.1; GSPDB:GN00020; CESP:T24249
A:Experimental source: clone B0491
R:Chui, C.
submitted to the EMBL Data Library, June 1995
A:Reference number: Z20004
A:Accession: T25249
A:Status: preliminary; translated from GB/EMBL/DBJ
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A:Residues: 1-1148 <W1>
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A:Experimental source: clone T24F1
C:Genetics:
A:Gene: CESP:T24F1.6
A:Map position: 2
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19621/3; 19648/3; 19675/3; 19702/3; 19729/3; 19756/3; 19783/3; 19810/3; 19837/3; 19864/3; 19891/3; 19918/3; 19945/3; 19972/3; 20000/3; 20027/3; 20054/3; 20081/3; 20108/3; 20135/3; 20162/3; 20189/3; 20216/3; 20243/3; 20270/3; 20297/3; 20324/3; 20351/3; 20378/3; 20405/3; 20432/3; 20459/3; 20486/3; 20513/3; 20540/3; 20567/3; 20594/3; 20621/3; 20648/3; 20675/3; 20702/3; 20729/3; 20756/3; 20783/3; 20810/3; 20837/3; 20864/3; 20891/3; 20918/3; 20945/3; 20972/3; 21000/3; 21027/3; 21054/3; 21081/3; 21108/3; 21135/3; 21162/3; 21189/3; 21216/3; 21243/3; 21270/3; 21297/3; 21324/3; 21351/3; 21378/3; 21405/3; 21432/3; 21459/3; 21486/3; 21513/3; 21540/3; 21567/3; 21594/3; 21621/3; 21648/3; 21675/3; 21702/3; 21729/3; 21756/3; 21783/3; 21810/3; 21837/3; 21864/3; 21891/3; 21918/3; 21945/3; 21972/3; 22000/3; 22027/3; 22054/3; 22081/3; 22108/3; 22135/3; 22162/3; 22189/3; 22216/3; 22243/3; 22270/3; 22297/3; 22324/3; 22351/3; 22378/3; 22405/3; 22432/3; 22459/3; 22486/3; 22513/3; 22540/3; 22567/3; 22594/3; 22621/3; 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25675/3; 25702/3; 25729/3; 25756/3; 25783/3; 25810/3; 25837/3; 25864/3; 25891/3; 25918/3; 25945/3; 25972/3; 26000/3; 26027/3; 26054/3; 26081/3; 26108/3; 26135/3; 26162/3; 26189/3; 26216/3; 26243/3; 26270/3; 26297/3; 26324/3; 26351/3; 26378/3; 26405/3; 26432/3; 26459/3; 26486/3; 26513/3; 26540/3; 26567/3; 26594/3; 26621/3; 26648/3; 26675/3; 26702/3; 26729/3; 26756/3; 26783/3; 26810/3; 26837/3; 26864/3; 26891/3; 26918/3; 26945/3; 26972/3; 27000/3; 27027/3; 27054/3; 27081/3; 27108/3; 27135/3; 27162/3; 27189/3; 27216/3; 27243/3; 27270/3; 27297/3; 27324/3; 27351/3; 27378/3; 27405/3; 27432/3; 27459/3; 27486/3; 27513/3; 27540/3; 27567/3; 27594/3; 27621/3; 27648/3; 27675/3; 27702/3; 27729/3; 27756/3; 27783/3; 27810/3; 27837/3; 27864/3; 27891/3; 27918/3; 27945/3; 27972/3; 28000/3; 28027/3; 28054/3; 28081/3; 28108/3; 28135/3; 28162/3; 28189/3; 28216/3; 28243/3; 28270/3; 28297/3; 28324/3; 28351/3; 28378/3; 28405/3; 28432/3; 28459/3; 28486/3; 28513/3; 28540/3; 28567/3; 28594/3; 28621/3; 28648/3; 28675/3; 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31729/3; 31756/3; 31783/3; 31810/3; 31837/3; 31864/3; 31891/3; 31918/3; 31945/3; 31972/3; 32000/3; 32027/3; 32054/3; 32081/3; 32108/3; 32135/3; 32162/3; 32189/3; 32216/3; 32243/3; 32270/3; 32297/3; 32324/3; 32351/3; 32378/3; 32405/3; 32432/3; 32459/3; 32486/3; 32513/3; 32540/3; 32567/3; 32594/3; 32621/3; 32648/3; 32675/3; 32702/3; 32729/3; 32756/3; 32783/3; 32810/3; 32837/3; 32864/3; 32891/3; 32918/3; 32945/3; 32972/3; 33000/3; 33027/3; 33054/3; 33081/3; 33108/3; 33135/3; 33162/3; 33189/3; 33216/3; 33243/3; 33270/3; 33297/3; 33324/3; 33351/3; 33378/3; 33405/3; 33432/3; 33459/3; 33486/3; 33513/3; 33540/3; 33567/3; 33594/3; 33621/3; 33648/3; 33675/3; 33702/3; 33729/3; 33756/3; 33783/3; 33810/3; 33837/3; 33864/3; 33891/3; 33918/3; 33945/3; 33972/3; 34000/3; 34027/3; 34054/3; 34081/3; 34108/3; 34135/3; 34162/3; 34189/3; 34216/3; 34243/3; 34270/3; 34297/3; 34324/3; 34351/3; 34378/3; 34405/3; 34432/3; 34459/3; 34486/3; 34513/3; 34540/3; 34567/3; 34594/3; 34621/3; 34648/3; 34675/3; 34702/3; 34729/3; 34756/3; 34783/3; 34810/3; 34837/3; 34864/3; 34891/3; 34918/3; 34945/3; 34972/3; 35000/3; 35027/3; 35054/3; 35081/3; 35108/3; 35135/3; 35162/3; 35189/3; 35216/3; 35243/3; 35270/3; 35297/3; 35324/3; 35351/3; 35378/3; 35405/3; 35432/3; 35459/3; 35486/3; 35513/3; 35540/3; 35567/3; 35594/3; 35621/3; 35648/3; 35675/3; 35702/3; 35729/3; 35756/3; 35783/3; 35810/3; 35837/3; 35864/3; 35891/3; 35918/3; 35945/3; 35972/3; 36000/3; 36027/3; 36054/3; 36081/3; 36108/3; 36135/3; 36162/3; 36189/3; 36216/3; 36243/3; 36270/3; 36297/3; 36324/3; 36351/3; 36378/3; 36405/3; 36432/3; 36459/3; 36486/3; 36513/3; 36540/3; 36567/3; 36594/3; 36621/3; 36648/3; 36675/3; 36702/3; 36729/3; 36756
```


F:421,422,423/Binding site: calcium (Asp, Gly, Asp) #status predicted

Query Match 3.1%; Score 175; DB 1; Length 946;
Best Local Similarity 18.6%; Pred. No. 0.0036;
Matches 158; Conservative 122; Mismatches 256; Indels 272; Gaps 36;
Qy 58 LVRKFSDEMNLRRKVEAVQNLVBAEADLNHEFNSLVFDYNSVLNERDEKGFV 117
Dy 154 LVRSSALDMEN-FTEVNVV---LPGAKVQFELHYQEVKRWKLGSEYHRIYLQPGRLAKHL 209
Qy 118 EL-----GAEFLLESN---AHFSNLPVNTSSVQLPTNVYVNDKPDILNGVYMSEAL 166
Dy 210 EVDVWVIEPQGLRFLHVPDTFEGHFGVPV---ISKQKQAHVSFK----- 252
Qy 167 NAVFVENFQRPDTLTWQYFGSATGFFRIYPIGKWTG-DENGVIITFDCRN-----R 215
Dy 253-----PTVAQO-----RIPCSECRETAVDGLVLYDVVKREKAGELVFN 292
Qy 216 GWYIOAATS-----PKDIVILVDVSGSMKGLRMTIAKHTITTLTDLTGENDFVNIAYN 269
Dy 293 GYFVHFAPDNLDPIPKNLFVIDVSGSMGVMKQVTEAMKTTLLDLRAEDHFSVIDFN 352
Qy 270 DYVHYIEPCFGILVQADNRNREHFKLLVEELMVKGVGVVDOALREAFQILKQFQBAKQG 329
Dy 353 QNTR-----TWNDLISATKTQVADAKRYIEKIQPSGGTNINEALLRAIFIL---NEANNL 405
Qy 330 SLCN-----QAIMLISDGAVEDYEPFBEKYNWPCDCKRVFTYLYIGREVSFADRMKIACNN 385
Dy 406 GLLDPNSVSLIILVSDG-----DPT-----VG-ELKLSKIQK----- 436
Qy 386 KGYTQISTLADTQENWVEYLHVLRSRPMVINHDHDIITWEAYMDSKLLSSQAQSLTLT 445
Dy 437-----NVKENIQDNISLFSLGMGFDVDYD----- 460
Qy 446 VAMPVFSKNETRSHGILLGVGSDVALRELMLKLAIPRYKLGVHGYAFINTNNGYILSHPD 505
Dy 461-----FLKRLSNENHGAQRIYGNQDTSQJLK-----FYNQ-----VSTPL 497
Qy 506 LRPL-----YREGKCLKPKPNYNSVDLSEVEMEDQAESLRTAMINR 546
Dy 498 LRNVQFNYPHTSVTDVTQNNFNHYPFGSGEIVVAGKPDPAKLQIESVITATSANTQLV-L 556
Qy 547 ETGTLSDVQKVPMDKGRV-----LFLTNDYFTDIDSPTFSLG-----AVLSRG 591
Dy 557 ETLAQMDLDQFLSKHADPDFTRKLWAYLTINQLLAERSLAPATAAKRRITRSILOMS 616
Qy 592 HGEVILLGNTSV-----EGLHDLHLPLDALAGDWIYCITDIDPDHRK----- 634
Dy 617 LDHIVTPLTSLVIENAGDERMLADAPPQDPPSCSGALYGVSKVDPDSTPSWANPSTP 676
Qy 635 -LSQLEAMIRPLTRKOPD-----LECDEELREVLFDAVVTAPMEAYWTALANMSESEH 689
Dy 677 VISMLAQGSQVLESTPPPHVMRVENDPHF-----IIVLPKQ--KNICFNIDSEPGK 726
Qy 690 VDMAFLGTAGLRSLFVGSEKVSQRKFLT-----PRD-----EASVFTLDRFPL 736
Dy 727 ILNLV-SDPESGIVVNGQLVGAKPNNGKLSYFGLGIFYQFQSEDIKIEISTETI----- 780
Qy 737 WYRQASHPAGSFVFNLRWREGPESAGEPMVVTVA--STAVAVTVDKRTATAAAGVOMKL 794
Dy 781-----TLSH--GSSTFSLWSWSDTAQVNTQNRQVQISVKKKCVTITLUDK-----EMSF 824
Qy 795 EFLQKFW 802
Dy 825 SVLLHRYW 832

RESULT 9

JC5575
Inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 09-Jul-2004
C;Accession: JC5575; PC4485

R;Nakatani, T.; Suzuki, Y.; Yamamoto, T.; Sinohara, H.

J. Biochem. 122, 71-82, 1997
A;Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors
sin inhibitor heavy chain family.
A;Reference number: JC5574; MUID:97420688; PMID:92766673
A;Accession: JC5575
A;Molecule type: mRNA
A;Residues: 1-946 <NAK>
A;Cross-references: UNIPROT:P97279; DDBJ:D89286; NID:G1694699; PIDN:BAAL3939.1; PID:G1616
A;Experimental source: liver
A;Accession: PC4485
A;Molecule type: protein
A;Residues: 55-64;140-146;151-156;424-447;500-528;577-605 <NA2>
C;Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3 were
that the complexes play important role for pancreatic cancer.
C;Superfamily: inter-alpha-trypsin inhibitor complex component II
F;261-264,717-916/Disulfide bonds: #status predicted

Query Match 3.0%; Score 172.5; DB 2; Length 946;
Best Local Similarity 23.3%; Pred. No. 0.0052;
Matches 90; Conservative 60; Mismatches 126; Indels 111; Gaps 18;
Qy 117 VEL-GAEFLLESN---AHFSNLPVNTSSVQLPTNVYVNDKPDILNGVYMSEALNAVFVE 172
Dy 216 VELQGRFLHVPDTFEGHFGVPV---ISKQKQKSHVSFK----- 252
Qy 173 NFORDPTLTWQYFGSATGFFRIYPIGKWTG-DENGVIITFDCRN-----RGWYIOA 221
Dy 253-----PTVAQO-----RKCPNCTYTAVDGLVVMYDVNREKVGLEVFNGYVHF 298
Qy 222 ATS-----PKDIVILVDVSGSMKGLRMTIAKHTITTLTDLTGENDFVNIAYNDYHYI 275
Dy 299 FAPENLDPIPKNLFVIDVSGSMGIMKQVTEAMKTTLLDLRTEDQFVVDVFNHNR-- 356
Qy 276 EPCFGKILVQADNRNREHFKLLVEELMVKGVGVVDOALREAFQILKQFQBAKQGLCN-- 333
Dy 357 --TWNDLISATKTQITDQRYIEKIQPSGGTNINEALLRAIFIL---NEASNLGMLNPD 411
Qy 334 --QAIMLISDGAVEDYEPV-----EKNMPDCKRVFTYLYIGREVSFADRMKW 380
Dy 412 SVSLIILVSDG-----DPTVGLKLSKIQKVNQKIQD-NISLFLSGIGFDVDY-DFLKR 464
Qy 381 IACNKGYYTQISTLADTQENWVEYLHVLRSRPMVIN-----HDH--- 419
Dy 465 LSNENRGAQRIYGNRDTSQLKFFYNQVSTPLLRNVQFNYPQASVTDVDTQNSFHNYPFG 524
Qy 420 -DIITWEAYMDSKLLSSQAQSLTLT 445
Dy 525 SEIVVAGKVDPSKL--AEVQSIITATS 549

RESULT 10

S54354
Inter-alpha-inhibitor H2 chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S54354
R;Chan, P.; Risler, J.L.; Raguenez, G.; Salier, J.P.
Biochem. J. 306, 505-512, 1995
A;Title: The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse:
A;Reference number: S54353; MUID:95194326; PMID:7534067
A;Accession: S54354
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-946 <CHA>
A;Cross-references: UNIPROT:Q61703; EMBL:X70392; NID:G695633; PIDN:CAA49842.1; PID:G6956;
C;Superfamily: inter-alpha-trypsin inhibitor complex component II

Query Match 2.9%; Score 166.5; DB 2; Length 946;
Best Local Similarity 23.4%; Pred. No. 0.013;
Matches 62; Conservative 52; Mismatches 84; Indels 67; Gaps 9;
Qy 225 PKDIVILVDVSGSMKGLRMTIAKHTITTLTDLTGENDFVNIAYNDYVHYIEPCFGILV 284

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Db 308 PKNLFVIDVSGSMGKMKQVTQAEAMKTIILDLRTDQFSVDFNHNVR-----TWNDIV 363
QY 285 QARDNRHFKLLVEELMVGVGVVDOALREAFQILKQFOEAKQSGSLCN-----QAIMLIS 340
Db 364 SATKQTQIADAKRYIEKIQPSGGNINEALLRAIFIL---NEASNMGLLNPDVSLIILVS 420
QY 341 DG-----AVEDYEPVPEKYNWPCCKVRVFTYLVIGREVSFADRMKWA 382
Db 421 DGBPTVGEELKSLQIKNVKSIQD-----NISLFSLGIGFDVY-DFLKRLS 466
QY 383 CNKNGYYTQISTLADTQENYMEYHLVSRPMVIN-----HDH-----D 420
Db 467 NENRGIAQRIYGNQDTSSQLKFKYQVNSTPLLRNVQPNYQASVTDVTQNNFHNFGSGE 536
QY 421 IINTEAWMDSKLLSSQAQSLTLTT 445
Db 527 IVVAGKFDPSKL--TEVQSIITATS 549

RESULT 11
JX0368
inter-alpha-trypsin inhibitor heavy chain-related protein precursor - human
N;Alternate names: IHRP; Plasma glycoprotein
C;Species: Homo sapiens (man)
C;Date: 22-Apr-1995 #sequence revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: JX0368; PC2355; S68457; S78548
R;Saguchi, K.; Tobe, T.; Hashimoto, K.; Sano, Y.; Nakano, Y.; Miura, N.H.; Tomita, M.
J. Biochem. 117, 14-18, 1995
A;Title: Cloning and characterization of cDNA for inter-alpha-trypsin inhibitor family H
A;Reference number: JX0368; MUID:95293915; PMID:7775381
A;Accession: JX0368
A;Molecule type: mRNA
A;Residues: 1-930 <SAG1>
A;Cross-references: UNIPROT:Q14624; DDBJ:D38595; NID:g664887; PIDN:BAA07602.1; PID:g1483
A;Accession: PC2355
A;Molecule type: protein
A;Residues: 29-44; 48-55; 61-75; 99-111; 140-151; 163-169; 211-224; 246-267; 274-281; 296-329; 392
A;Experimental source: liver
R;Nishimura, H.; Kakizaki, I.; Muta, T.; Sasaki, N.; Pu, P.X.; Yamashita, T.; Nagasawa,
FEBS Lett. 357, 207-211, 1995
A;Title: cDNA and deduced amino acid sequence of human PK-120, a plasma kallikrein-sensi
A;Reference number: S68457; MUID:95104473; PMID:7805892
A;Accession: S68457
A;Molecule type: mRNA
A;Residues: 1-84, 'I', 86-113, 'S', 115-930 <NIS>
A;Cross-references: EMBL:D38535; NID:g624879; PIDN:BAA07536.1; PID:g1402590
A;Accession: S78548
A;Molecule type: protein
A;Residues: 29-45; 171-184; 211-239; 274-281; 301-315; 429-443; 488-502; 690-695; 697-700; 703-72
A;Experimental source: liver
C;Comment: The amino-terminal 600 residues exhibits homology with those of inter-alpha t
C;Function:
A;Description: highly sensitive to plasma kallikrein
C;Superfamily: inter-alpha-trypsin inhibitor complex component II
C;Keywords: chondroitin sulfate proteoglycan; glycoprotein; serine proteinase inhibitor
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-687/Product: inter-alpha trypsin inhibitor heavy chain-related protein #status pred
F;688-930/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;81,207,517/Binding site: carboxylate (Asn) (covalent) #status predicted
F;666/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted
F;696,702/Binding site: carboxylate (Ser) (covalent) #status predicted
F;701/Binding site: carboxylate (Thr) (covalent) #status predicted

Query Match 2.9%; Score 164.5; DB 2; Length 930;
Best Local Similarity 19.0%; Pred. No. 0.017;
Matches 147; Conservative 118; Mismatches 313; Indels 195; Gaps 31;

QY 26 NTVTKYSGSLLOKQYKDVESLUKIEVDGLVLRKFSF-----DNEANML 70
Db 62 NTVQETATFQWELPKKAFITNFSNIDGMYPGIIKKAQAQYSAVAKGNAGLVKAT 121
QY 71 RRKVEAVQNLEAAEADLNHEFNESLVFDYNSVNLINERDEKGNFVELGAFFLESNAH 130
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Db 122 GRNMEQFOYSVSVAPNAKTIFE-----LVYE-----ELKKR-----LGVYELL----- 160
QY 131 FSNLPNTSISSVOLPTNVNKKDPDILNGVYMSEALNAVFNQFDRPDLTWQYFGSATG 190
Db 161 ---LKVRPQOLVKHLQMDIHIFEP---QGISFLET-ESTFMTNLQVDAULTWQ--NKTKA 211
QY 191 FRRIYPGI-----KWTDPENGVIITFDCR-----NRGWYIQ-----AATS 224
Db 212 HIRFKETLSQOQSPQOQETVLDGNLIIRYVDVDRRAISGSGIQIENGIFYVHFAPGGLTMM 271
QY 225 PKDIVILVDVSGSMKGLRMTIAKHHTITTLTDLTGLDGFVNIIAYNDVHYIEBCEKGLV 284
Db 272 PKNVFVVDKSGSMGRKIQOTREALIKILLDLSPRDQFNLIIVFESTEATQWRES----LV 327
QY 285 QARDNRHFKLLVEELMVGVGVVDOALREAFQIL---KQFOEAKQSGSLCNQAIMLISD 341
Db 328 PASAENVNKRSPFAAGIQALGGTINIDAMLMVQLDSSNQBEERLPEGSV--SLIILLTD 385
QY 342 G--AVEDYEPVPEKYNWPCD---KVRVFTYLVIGREVSFADRMKWAICNNKNGYTOISTLA 396
Db 386 GDBPTVGETNPRSIQNNVREAVSGRYSIFCLGFGFVSYAFLEK-LALDNGGLARRIHEDS 444
QY 397 DTQENYMEYHLVSRPMVINHDHDIITWYAYMDSKLLSSQAQSLTLTTTVAMPVFSKKN 456
Db 445 DSALQLQDFQVEVANPLL-----TAVTFEYPSNAVEEVTONNFRLLFKGSEMVVAGLKQ 498
QY 457 TRSHGILLGVVG-----SDVALRELMLKLAAPRY-----KLGVH----- 488
Db 499 DRGPDVLTATVSGKLPQTQNTITQTESVAEAEFQSPKYIFHNFMERLWAYLTIQOLLE 558
QY 489 -----GYAFLTNNGVILSHPD-----LRPL----- 509
Db 559 QTVSASDAQALRQALNQLNLSAYSVTPLTSMVVTKPDQEQSQAEPMEGESNRNV 618
QY 510 -----YREGKKL-KPKPNYNSVDLSEWEQAESLRTAMINRETGTLS---MDVK 556
Db 619 HSGSTPFKYVLQCAKIPKEASFS---PRRGWNRQAGAAGSRM-NFRPGVLSRQLGLP 673
QY 557 VPMDKGKRVLFTNDYFFDDISDTPSLCAVLSRGHGEVILLGNTSVREGLHLLHPD-- 614
Db 674 GPPDPVDDHAAY---HPFRRLAILPASAPPATSNPDPAVSRVMNMKIEETMTTQTQPAPI 729
QY 615 -----LALAGDWIYCIITIDPDHRLKLSQLEAMIRFLTRKDPDLECDCEELVRE 661
Db 730 QAPSAILPLPGOSVERLC-VDPHRH-----QGPVNLSDPEQGVETGQYERE 776

RESULT 12
JCS576
inter-alpha-trypsin inhibitor heavy chain 3 - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 17-Mar-1999
C;Accession: JCS576; PC4486
R;Nakatani, T.; Suzuki, Y.; Yamamoto, T.; Sinohara, H.
J. Biochem. 122, 71-82, 1997
A;Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors
sin inhibitor heavy chain family.
A;Reference number: JCS574; MUID:97420688; PMID:92766673
A;Accession: JCS576
A;Molecule type: mRNA
A;Residues: 1-889 <NAK>
A;Cross-references: DDBJ:D89287
A;Experimental source: liver
A;Accession: PC4486
A;Molecule type: protein
A;Residues: 34-53; 449-475; 509-526 <NA2>
C;Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3 were
that the complexes play important role for pancreatic cancer.
C;Superfamily: inter-alpha-trypsin inhibitor complex component II
F;236-239,664-865/Disulfide bonds: #status predicted

Query Match 2.6%; Score 150.5; DB 2; Length 889;
```


F;647/Modified site: chondroitin sulfate ester carboxyl end (Asp) (in mature form) #stad		
Query Match 2.6%; Score 146.5; DB 2; Length 885; Best Local Similarity 21.9%; Pred. No. 0.24; Matches 73; Conservative 63; Mismatches 147; Indels 51; Gaps 14;		
QY	118 ELGAEFLLENAHPSNLPVNTSSVOLPTNVYKDPDIL--NGVYSEALNAVVENFQ 175	
DB	149 ELTYEELK--RHKGKYTEMLKQPKLVKH-PBIEVDIFEPGIGISMLDA-EASFITNDL 204	
QY	176 RDPFLTQWYFGSATGPRFPIYGIKWTPDE-----NG-VITPCRN----- 214	
DB	205 LGSALT-KSFSGKGHVSFRPSL-----DQORSCPCTDSSLINGDTITYDNNRESPGVQ 259	
QY	215 --RGWYIQ-----AATSPKDIIVLDVSGSMGLRMTIAKHTTTITDITLGENDFVNII 266	
DB	260 IVNGYFVHPAPQGLPVVKNVAFVIDISGMAGRKLEQTKEALLRILEDMQBEDYLNFI 319	
QY	267 AYNDYVHYIEPCFKGILVQADRONREHFKLLVELMVKGV-GVVDAQALREAFQILKQFOE 325	
DB	320 LFGSDV---STWKEHLVQATPENLQBAKTFVKSMEDKGMTINIDGILLGISMINKAREE 375	
QY	326 AKQSLCNQAIMLISDGAVEDYSPVEKY-----NWPDCKVRVFTYILIGREVSFADRMKW 380	
DB	376 HRIPERSTSIWMTDGDANVGSRPEKIQENVRNAIGGRFPLYNLGFGNNLAY-NPLEN 434	
QY	381 IACNKGYYTQISTLADTQENVMYHLVLSRPMV 414	
DB	435 MALENHGFARRIYEDSDADLQLQGFYEVANPLL 468	
RESULT 15		
A90551		
conserved hypothetical protein MYPJ_3130 [imported] - Mycoplasma pulmonis (strain UAB CT		
C;Species: Mycoplasma pulmonis		
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004		
C;Accession: A90551		
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Sanson, D.; Galisson, F.; Moszer, I.;		
Nucleic Acids Res. 29, 2145-2153, 2001		
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm		
A;Reference number: A9512; MUID:21267165; PMID:11353084		
A;Accession: A90551		
A;Status: preliminary		
A;Molecule type: DNA		
A;Residues: 1-2819 <KUR>		
A;Cross-references: UNIPROT:Q98Q96; GB:AL445566; PID:g14089727; PIDN:CAC13486.1; GSPDB:G		
A;Experimental source: strain UAB CTIP		
C;Genetics:		
A;Gene: MYPJ_3130		
A;Genetic code: SGC3		
Query Match 2.5%; Score 145.5; DB 2; Length 2819;		
Best Local Similarity 18.7%; Pred. No. 1.9;		
Matches 154; Conservative 130; Mismatches 261; Indels 279; Gaps 41;		
QY	41 YKDVESSLKIEEVDGLERK-----FSEDMMMLRRKVEAVQ--NLVEAAEEADLN-HEF 93	
DB	733 FYEVSKTL-VNIVDTLELLEKVLKFIIEIKSSAQLKLSNPKFNLIEKLOKSIISTFGF 791	
QY	94 NESLIFDYNSVL-----INERDEKGNFVELGAEFLLESNAHFNL--PVNTSISVVQ 144	
DB	792 TNDLGSFLKQVVKSKSLSSVEQDKFTSSLKEVSVFVKSENKVLSSAGTYLSNIE 851	
QY	145 LPTNVYKDPDILNGVYSEALNAVVENFQDPTL-----TWQYFGSATGFPI 194	
DB	852 L-----FAENSDVPKGFPS-----HILNFKETPELLNKIIDYVINSWESIDQYNDAFEP 900	
QY	195 YPGIKWTPDENGVTTCRNRGWYIQATSPKDI---VILVDVS-----GSMK 239	
DB	901 -----VILFLKTSSWF---KTVVKDIFSSVNVSEIQYANILTSKLKLSQA 945	
QY	240 GLRMT-----IA-KHTITILD-----TLGENDFVNIIAYNDVHYI 275	

DB	946 GFELTNSSVESIKNIETNTLKIIADSNITDALVDFTFVNSKTLLEIDKKNPFA----- 997	
QY	276 EPCFKGILVQADRDNR--BHFKLLVBEELMVKGVGVVDQALREAFQILKQ--FOEAKQGS 331	
DB	998 --SLKNIQIFALSDDDNPFVFKALISSNKLKOKAFVNYQYKQDITNVLKELLPE----- 1049	
QY	332 CNOAIMLISDGAVEDYEPVEKYNWPDCKVRVFTYILIGR-----EVSFADRMKWIACNNK 386	
DB	1050 --KFFNLIYSFMMPKTSELFE--NNPEALNKTTTILRNALKKNDLPDFINKMMDIIFDNL 1105	
QY	387 GYTYQTIST-----LADTQENVMYHLVLSRPMVINHD-HDI1-----WTEAYWDSK 431	
DB	1106 DKYQKULENTGVQGLILKDNDSDAIATKQVAFKDVVNEANFQDVLKVLVLSQTKFMGFE 1165	
QY	432 LLSQAQSL-TLITTTVAMPVFSKNETRSHGILLGVVGSVALRELMLKAPRYKLGVHG 490	
DB	1166 LNADETINKISTDLTKILKQVFESNNEFAS-----LALATKDSLVIDGV 1208	
QY	491 -----AFUNTNNGVILSHPDRLRPLYREGKCLKPKPNYSV----DLSVEVWEDQA 536	
DB	1209 QANKKIFDPTFRFLNT---ELLSEK-----EKTKENYQMKVKSILNTKLIDISQNS 1255	
QY	537 ESLRTAMINRETGTLTSM-----VKVPMDKGKRVLFLTNDYFF-----TDISD- 579	
DB	1256 ESINKLLTFTKSALSRSRDEFYEKTIKVLSEKELASAYTPVVEFVKVLNKEKTTNFSOL 1315	
QY	580 -----TPFS-----LGAVLS- 589	
DB	1316 LIDSLFKDFSQYQANSFELIYLVLRNNKETVNVYLKELSPKSSNIIQRLLGQTINA 1375	
QY	590 --RGHGEYI-----LLGNTSVBEGLDHLLHPDLALAGDWIYCYTID 629	
DB	1376 LVTPNGEKIFSDTELQSLSTLINESLDLFGKTNIIISNLDVLVSALSINQESSSVLTKE 1435	
QY	630 P-DHRKLSQLE--AMIR-FLTRKQPDLECDSELYREVLFDVV 668	
DB	1436 NITHKALDQONSFYFAVIKTLTLLSVKEGVDKSDS-----FKAI 1473	

Search completed: November 16, 2005, 03:24:34
Job time : 54 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 03:12:42 ; Search time 188 Seconds
(without alignments)

2968.970 Million cell updates/sec

Title: US-09-833-222a-10

Perfect score: 5726

Sequence: 1 MAVALGTRRRDRVRLWADTF.....MPNMTVPVLLGGNIRVYAL 1090

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5399.5	94.3	1120	2	Q81ZS9
2	5373.5	93.8	1137	2	Q7Z3S7
3	4649	81.2	974	2	Q7Z3S8
4	3422	59.8	1091	2	Q9Z1L5
5	3416.5	59.7	1091	2	Q81ZS8
6	3410	59.6	1085	2	Q8CFG5
7	3250.5	56.8	997	2	Q9NY16
8	1866.5	32.6	519	2	Q9NY18
9	1551	27.1	1218	2	Q9V6T7
10	1496.5	26.1	1170	2	Q81P22
11	1441	25.2	2190	2	Q9VJM0
12	1430.5	25.0	1028	2	Q7Q758
13	1398	24.4	1011	2	Q7PM00
14	1305.5	22.8	1255	2	Q9NK83
15	1283	22.4	1120	2	Q9VJN7
16	1262	22.0	394	2	Q8AVV7
17	1243	21.7	967	2	Q7PM11
18	1189	20.8	1098	2	Q8CEH9
19	1183.5	20.7	1076	2	Q9U5W0
20	1183.5	20.7	1145	2	Q9Y268
21	1182.5	20.7	1157	2	Q8CFG6
22	1182	20.6	1084	2	Q920H6
23	1182	20.6	1156	2	Q9EQG2
24	1180	20.6	1148	2	Q8C8R8
25	1174.5	20.5	1143	2	Q9NY48
26	1173	20.5	1154	2	Q6PHS9
27	1171.5	20.5	1186	2	Q6REE3
28	1171	20.5	1150	2	Q9NY47
29	1109	19.4	1084	2	Q8CFG7
30	1106.5	19.3	1103	1	C1C2 MOUSE
31	1105.5	19.3	1091	2	Q9ER53

32	1101.5	19.2	1079	2	Q8VHS9
33	1090	19.0	1091	2	Q77773
34	1089	19.0	975	2	Q7Z6Z1
35	1089	19.0	1106	1	C1C2 RABIT
36	1078	18.8	1110	2	Q9UIU0
37	1077.5	18.8	1091	1	C1C2 HUMAN
38	1056.5	18.5	1091	1	C1C3_RAT
39	949.5	16.6	204	2	Q86XZ5
40	935.5	16.3	842	2	Q9SR75
41	705	12.3	1249	1	UN36 CAEEL
42	672.5	11.7	745	2	Q9UDQ3
43	543	9.5	1067	2	Q17517
44	543	9.5	1067	2	Q7JMF9
45	452	7.9	140	2	Q8JFPR4

ALIGNMENTS

RESULT 1

Q81ZS9 PRELIMINARY; PRT; 1120 AA.

ID Q81ZS9
AC Q81ZS9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Voltage-gated calcium channel alpha(2)delta-4 subunit.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22169250; PubMed=12181424;
RA Qin N., Yagel S., Mompalao M.L., Codd E.E., D'Andrea M.R.;
RT "Molecular cloning and characterization of the human voltage-gated
RT calcium channel alpha(2)delta-4 subunit."
RL Mol. Pharmacol. 62:485-496(2002).
DR EMBL; AF516695; AA006672.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 2.
DR Pfam; PF00092; VWA; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS0234; VWF_A; 1.
SQ SEQUENCE 1120 AA; 126204 MW; 4F950C11C3249984 CRC64;

Query Match		94.3%	Score 5399.5;	DB 2;	Length 1120;
Best Local Similarity		98.2%	Pred. No. 0;		
Matches 1035;		Conservative 5;	Mismatches 11;	Indels 3;	Gaps 2;
Qy	11	DRVKLWADTFGGDLYNTVTYKSGSLLLQKKYKDVESLSLKEEVDGLVLRKFSDEMML	70		
Db	58	ETVKLWADTFGGDLYNTVTYKSGSLLLQKKYKDVESLSLKEEVDGLVLRKFSDEMML	117		
Qy	71	RRKVEAVQNLEAAEEADLNHEFNESLSVFDYNSVLINERDEKGNFVLCGAEFLLESNAH	130		
Db	118	RRKVEAVQNLEAAEEADLNHEFNESLSVFDYNSVLINERDEKGNFVLCGAEFLLESNAH	177		
Qy	131	FSNLPNTSISSVQLPTNTYKNDPDLINGVYNSALNAVFNFORPTLTWQYFGSATG	190		
Db	178	FSNLPNTSISSVQLPTNTYKNDPDLINGVYNSALNAVFNFORPTLTWQYFGSATG	237		
Qy	191	FRIRYPGIKWTDPDENGVIITFCNCRGWYIQAAATSPKDIIVLDVSGSMKGLRMTIAKHTI	250		
Db	238	FRIRYPGIKWTDPDENGVIITFCNCRGWYIQAAATSPKDIIVLDVSGSMKGLRMTIAKHTI	297		
Qy	251	TTILDTLGENDFVNIITAYNDYVHYIEPCFKGILVQADRNREHFHFKLLVEELMVKGVGVD	310		
Db	298	TTILDTLGENDFVNIITAYNDYVHYIEPCFKGILVQADRNREHFHFKLLVEELMVKGVGVD	357		
Qy	311	QALREAFQILKQFEAKQCSLNCQAIMLISDGAVEDYEPVFEKYNWPCDKVRVFTYLIGR	370		

Db 358 QALREAFQILKQFOEAKQSSLCNQAIWLIISDGAVEDYEPVEKYNWDCVKRVFTYLIGR 417
 Qy 371 EVSPADRMKIACNNKGYTQISTLATQENWMEYLHLVSRPMVINHDHDIWTEAYMDS 430
 Db 418 EVSPADRMKIACNNKGYTQISTLATQENWMEYLHLVSRPMVINHDHDIWTEAYMDS 477
 Qy 431 KLLSSQAQSLTLTTVAMPVFSKKNETRSKNGIILGVVGSVALRELKMLAPRYKLGHVGY 490
 Db 478 KLLSSQAQSLTLTTVAMPVFSKKNETRSKNGIILGVVGSVALRELKMLAPRYKLGHVGY 537
 Qy 491 AFLNTNNGYILSHPDRLPLRYREGKLLKPKPNYNSVDLSEVEWDOAESLRTAMINRETGT 550
 Db 538 AFLNTNNGYILSHPDRLPLRYREGKLLKPKPNYNSVDLSEVEWDOAESLRTAMINRETGT 597
 Qy 551 LSHMDVKVPMDKGRVLFNTDYFTDIDSDTFFSLGAVLSRGHGEYILLGNSTVEEGLHDL 610
 Db 598 LSHMDVKVPMDKGRVLFNTDYFTDIDSDTFFSLGAVLSRGHGEYILLGNSTVEEGLHDL 657
 Qy 611 LHPDLALAGDWIYICITDIDPDHRLKLSQLEAMIRFLTRKDPDLECEBELVREVLFDVAVTA 670
 Db 658 LHPDLALAGDWIYICITDIDPDHRLKLSQLEAMIRFLTRKDPDLECEBELVREVLFDVAVTA 717
 Qy 671 PMEAYWTALALNMSSESEHVVDMFLGTRAGLLRSSLFGSEKVSQRKFLTPDEASVFT 730
 Db 718 PMEAYWTALALNMSSESEHVVDMFLGTRAGLLRSSLFGSEKVSQRKFLTPDEASVFT 777
 Qy 731 LDRFPPLWYRQASEHPAGSFVFNLRWAEKPSAGEPMVVTASTAVATVDRKTAIAAAGV 790
 Db 778 LDRFPPLWYRQASEHPAGSFVFNLRWAEKPSAGEPMVVTASTAVATVDRKTAIAAAGV 837
 Qy 791 QMKLEFLQRFKWAATRCQSTVDGPYTQSCDSLDLCEVINDNNGFILLIKSRSTGRFLGE 850
 Db 838 QMKLEFLQRFKWAATRCQSTVDGPYTQSCDSLDLCEVINDNNGFILLIKSRSTGRFLGE 897
 Qy 851 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHSAAQPLVSPISAFATATRWLLQELVL 910
 Db 898 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHSAAQPLVSPISAFATATRWLLQELVL 957
 Qy 911 FLEWSVMGSWYDRGAEAKSVFHHSHKHKKQDPLOPCDTEYPVVFVQPAIRANGIVECG 970
 Db 958 FLEWSVMGSWYDRGAEAKSVFHHSHKHKKQDPLOPCDTEYPVVFVQPAIRANGIVECG 1017
 Qy 971 PCQKVFVQVQIPNSNLLLVTDPTCDCSIPPPVLQATEVKYNASVKCDMRMSQKLRRRP 1030
 Db 1018 PCQKVFVQVQIPNSNLLLVTDPTCDCSIPPPVLQATEVKYNASVKCDMRMSQKLRRRP 1077
 Qy 1031 DSCHAFHPEVRVBRADRGWAGFSNP--LCLGLC 1062
 Db 1078 DSCHAFHPEENAQ-DCGGASDTSASPPLLLPVC 1110

RESULT 2

Q723S7
 ID Q723S7 PRELIMINARY; PRT; 1137 AA.
 AC Q723S7;
 DT 01-OCT-2003 (T-EMBLrel. 25, Created)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Hypothetical protein DKF2p686O0495.
 GN Name=DKF2p686O0495;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa;
 OC Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human retina;
 RA Bloembergen H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobio G., Han M., Wiemann S.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX537437; CAD97679.1; -;
 GO; GO:0016020; C:membrane; IEA.

DR InterPro: IPR004010; Cache.
 DR InterPro: IPR002035; VMP_A.
 DR Pfam: PF02743; Cache; 2.
 DR Pfam: PF00092; VMA; 1.
 DR SMART: SM00327; VMA; 1.
 DR PROSITE: PS0234; VMA; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 1137 AA; 127965 MW; 69410B72580F3FF7 CRC64;
 Query Match 93.8%; Score 5373.5; DB 2; Length 1137;
 Best Local Similarity 97.8%; Pred. No. 1.6e-317;
 Matches 1031; Conservative 5; Mismatches 15; Indels 3; Gaps 2;
 Qy 11 DRVKLWADTFGGDLVNTVTKYSGSLLLQKKYKDVSSSLKIEEVDGLELVKRFKPSDEMNML 70
 Db 75 ETVKLWADTFGGDLVNTVTKYSGSLLLQKKYKDVSSSLKIEEVDGLELVKRFKPSDEMNML 134
 Qy 71 RRRKVEAVQNQLVEAAEADLNHFENESLVFDYNSVLINERDEKGNFVELGAEFLLESNAH 130
 Db 135 RRRKVEAVQNQLVEAAEADLNHFENESLVFDYNSVLINERDEKGNFVELGAEFLLESNAH 194
 Qy 131 FSNLPVNTSISSVQLPTNTVYKDPDILNGVYMSALNAVVENFQDDPTLTWQYFGSATG 190
 Db 195 FSNLPVNTSISSVQLPTNTVYKDPDILNGVYMSALNAVVENFQDDPTLTWQYFGSATG 254
 Qy 191 FRIYPIGIKWTDPENGVIITDCRNRGWYIOAATSPKDIIVLDVSGSMKGLRMTIAKHTI 250
 Db 255 FRIYPIGIKWTDPENGVIITDCRNRGWYIOAATSPKDIIVLDVSGSMKGLRMTIAKHTI 314
 Qy 251 TTILDTLGENDFVNIITAYNDYVHYIIEPCFKGILVQADRDNRHFKLLVEELVMKGVGVND 310
 Db 315 TTILDTLGENDFVNIITAYNDYVHYIIEPCFKGILVQADRDNRHFKLLVEELVMKGVGVND 374
 Qy 311 QALREAFQILKQFOEAKQSSLCNQAIWLIISDGAVEDYEPVEKYNWDCVKRVFTYLIGR 370
 Db 375 QALREAFQILKQFOEAKQSSLCNQAIWLIISDGAVEDYEPVEKYNWDCVKRVFTYLIGR 434
 Qy 371 EYSPADRMKIACNNKGYTQISTLATQENWMEYLHLVSRPMVINHDHDIWTEAYMDS 430
 Db 435 EYSPADRMKIACNNKGYTQISTLATQENWMEYLHLVSRPMVINHDHDIWTEAYMDS 494
 Qy 431 KLLSSQAQSLTLTTVAMPVFSKKNETRSKNGIILGVVGSVALRELKMLAPRYKLGHVGY 490
 Db 495 KLLSSQAQSLTLTTVAMPVFSKKNETRSKNGIILGVVGSVALRELKMLAPRYKLGHVGY 554
 Qy 491 AFLNTNNGYILSHPDRLPLRYREGKLLKPKPNYNSVDLSEVEWDOAESLRTAMINRETGT 550
 Db 555 AFLNTNNGYILSHPDRLPLRYREGKLLKPKPNYNSVDLSEVEWDOAESLRTAMINRETGT 614
 Qy 551 LSHMDVKVPMDKGRVLFNTDYFTDIDSDTFFSLGAVLSRGHGEYILLGNSTVEEGLHDL 610
 Db 615 LSHMDVKVPMDKGRVLFNTDYFTDIDSDTFFSLGAVLSRGHGEYILLGNSTVEEGLHDL 674
 Qy 611 LHPDLALAGDWIYICITDIDPDHRLKLSQLEAMIRFLTRKDPDLECEBELVREVLFDVAVTA 670
 Db 675 LHPDLALAGDWIYICITDIDPDHRLKLSQLEAMIRFLTRKDPDLECEBELVREVLFDVAVTA 734
 Qy 671 PMEAYWTALALNMSSESEHVVDMFLGTRAGLLRSSLFGSEKVSQRKFLTPDEASVFT 730
 Db 735 PMEAYWTALALNMSSESEHVVDMFLGTRAGLLRSSLFGSEKVSQRKFLTPDEASVFT 794
 Qy 731 LDRFPPLWYRQASEHPAGSFVFNLRWAEKPSAGEPMVVTASTAVATVDRKTAIAAAGV 790
 Db 795 LDRFPPLWYRQASEHPAGSFVFNLRWAEKPSAGEPMVVTASTAVATVDRKTAIAAAGV 854
 Qy 791 QMKLEFLQRFKWAATRCQSTVDGPYTQSCDSLDLCEVINDNNGFILLIKSRSTGRFLGE 850
 Db 855 QMKLEFLQRFKWAATRCQSTVDGPYTQSCDSLDLCEVINDNNGFILLIKSRSTGRFLGE 914
 Qy 851 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHSAAQPLVSPISAFATATRWLLQELVL 910
 Db 915 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHSAAQPLVSPISAFATATRWLLQELVL 974

```
Qy 911 FLEWSVWGSDYDRGAEAKSVFHHSHKHKQDPLQPCDTEVPVYQPAIREANGIVECG 970
Db 975 FLEWSVWGSDYDRGAEAKSVFHHSHKHKQDPLQPCDTEVPVYQPAIREANGIVECE 1034
Qy 971 PCQKVFVVOQIPNSNLVLLVTDPTCDSCSIPPPVLOEATEVKYNASVKCDRMRSKLRRRP 1030
Db 1035 PCQKVFVVOQIPNSNLVLLVTDPTCDSCSIPPPVLOEATEVKYNASVKCDRMRSKLRRRP 1094
Qy 1031 DSHAFPEVRVEADRGWAGFSNP--LCILGLC 1062
Db 1095 DSHAFPEENAQ--DCGASDTSAPPLILLPVC 1127

RESULT 3
Q723S8
ID Q723S8 PRELIMINARY; PRT; 974 AA.
AC Q723S8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Hypothetical protein DRF2P686A1395.
GN Name=DKF2P686A1395;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human retina;
RA Bloecher H., Boscher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX537436; CAD97678.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 2.
DR Pfam; PF00092; VWA; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50234; VWA; 1.
KW Hypothetical protein.
SQ SEQUENCE 974 AA; 109568 MW; 6F3C91CD0A038ED2 CRC64;

Query Match 81.2%; Score 4649; DB 2; Length 974;
Best Local Similarity 99.4%; Pred. No. 1.3e-273;
Matches 895; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 11 DRVKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESLKIIEVDGLVLRKFSDEMML 70
Db 75 ETVKWADTFGGDLYNTVTKYSGSLLLQKKYKDVESLKIIEVDGLVLRKFSDEMML 134

Qy 71 RRYEAVQNLVEAAEADLNHEPNESLVFDYNSVLINERDEKGNFVELGAEPFLLENAH 130
Db 135 RRYEAVQNLVEAAEADLNHEPNESLVFDYNSVLINERDEKGNFVELGAEPFLLENAH 194

Qy 131 FSNLPVNTSISVOLPTNVYKOPDILNGVYMSALNAVVFENQRPDPTLWYFGSATG 190
Db 195 FSNLPVNTSISVOLPTNVYKOPDILNGVYMSALNAVVFENQRPDPTLWYFGSATG 254

Qy 191 FFRIYPGIKWTPDNGVITFCRNRGWYIQAATSPKDIIVLVDSGSMKGLRMTIAKHTI 250
Db 255 FFRIYPGIKWTPDNGVITFCRNRGWYIQAATSPKDIIVLVDSGSMKGLRMTIAKHTI 314

Qy 251 TTILDTLGENDFVNIIVNDVHYIEPCFKGILVQADRNRHEPKLLVEELMWKGVGVVD 310
Db 315 TTILDTLGENDFVNIIVNDVHYIEPCFKGILVQADRNRHEPKLLVEELMWKGVGVVD 374

Qy 311 QALREAFQILKQFEAKQGSGLCNQAIMLISDGAVEDYEPFEKYNWPDCKVRVFTYLIGR 370
Db 375 QALREAFQILKQFEAKQGSGLCNQAIMLISDGAVEDYEPFEKYNWPDCKVRVFTYLIGR 434

Qy 371 EVSFADRMKWIACNNKGYTQISTLATQENVMYHLVLSRPMVINHHDDIIWTEAYNDS 430
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Db 435 EVSFADRMKWIACNNKGYTQISTLATQENVMYHLVLSRPMVINHHDDIIWTEAYNDS 494
Qy 431 KLASQASQSLTLTTVAMPVFSKKNETRSRGILLGVVGSVDVALRELKMLAPRYKLGVRHG 490
Db 495 KLASQASQSLTLTTVAMPVFSKKNETRSRGILLGVVGSVDVALRELKMLAPRYKLGVRHG 554
Qy 491 AFLNTNNGYILSHPDPLPLREGKKLPKPNYSVDLSEVEWEOAQSRLRTAMINRETGT 550
Db 555 AFLNTNNGYILSHPDPLPLREGKKLPKPNYSVDLSEVEWEOAQSRLRTAMINRETGT 614
Qy 551 LSHMDVKVPMDKGRKVLFLTNDYFFTDISDPFSLGAVLSRGHGYYILLGNTSVBEGHDL 610
Db 615 LSHMDVKVPMDKGRKVLFLTNDYFFTDISDPFSLGAVLSRGHGYYILLGNTSVBEGHDL 674
Qy 611 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRELTRKDPDLECEELVRELVFADVTA 670
Db 675 LHPDLALAGDWIYCITDIDPDHRKLSQLEAMIRELTRKDPDLECEELVRELVFADVTA 734
Qy 671 PMEAYWTALALNMSESESEHVVDMAFLGTRAGLLRSSLPVSGSEKYSDRKFLTPEDASVFT 730
Db 735 PMEAYWTALALNMSESESEHVVDMAFLGTRAGLLRSSLPVSGSEKYSDRKFLTPEDASVFT 794
Qy 731 LDRFPLWYRQASEHPAGSFVFNLRWAGSPSAGSPMVVTAATAVAVTVDKRTATAAAAGV 790
Db 795 LDRFPLWYRQASEHPAGSFVFNLRWAGSPSAGSPMVVTAATAVAVTVDKRTATAAAAGV 854
Qy 791 QMKLEFLQRFWAATRCSTVDGPTQSCDSLDLCFVIDNNGFILSKRSRTRGRFLGE 850
Db 855 QMKLEFLQRFWAATRCSTVDGPTQSCDSLDLCFVIDNNGFILSKRSRTRGRFLGE 914
Qy 851 VDGAVALTQLLSMGVFSQVMTDYQAMCKPSHHSHHSAAPLSPISAFJATATRWLLQELVL 910
Db 915 VDGAVALTQLLSMGVFSQVMTDYQAMCKPSHHSHHSAAPLSPISAFJATATRWLLQELVL 974

RESULT 4
Q921L5
ID Q921L5 PRELIMINARY; PRT; 1091 AA.
AC Q921L5;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Calcium channel alpha-2-delta-C subunit.
GN Name=Cacna2d3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Klugbauer N., Lacinova L., Marais E., Hobom M., Hofmann F.;
RT "Molecular diversity of the calcium channel alpha2delta subunit.";
RL J. Neurosci. 19:648-691(1999).
DR EMBL; AJ010949; CAA09423.1; -.
DR PIR; T30256; T30256.
DR MG; MG:1338890; Cacna2d3.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 2.
DR Pfam; PF00092; VWA; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50234; VWA; 1.
SQ SEQUENCE 1091 AA; 122777 MW; 7AE2BDA10077A0A CRC64;
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Query Match 59.8%; Score 3422; DB 2; Length 1091;
Best Local Similarity 60.0%; Pred. No. 5.5e-199;
Matches 627; Conservative 188; Mismatches 212; Indels 18; Gaps 6;

Qy 13 VKLWADTFGGDLYNTVTKYSGSLLLQKKYKDVESLKIIEVDGLVLRKFSDEMMLR 72
Db 42 VKLWASAFGGEIKSIAAKYSGSQLQKKYKDYKDVAEIEIDGLQVKKLAKIMEPFHK 101
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DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Calcium channel alpha2-delta3 subunit.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=21142395; PubMed=11245980; DOI=10.1016/S0378-1119(00)00600-4;
RA Hanke S., Bugert P., Chudek J., Kovacs G.;
RT "Cloning a calcium channel alpha2delta-3 subunit gene from a putative
RT tumor suppressor gene region at chromosome 3p21.1 in conventional
RT renal cell carcinoma.";
RL Gene 264:69-75(2001).
DR EMBL; AJ272268; CAB75962.1; -.
DR GenBank; HGNC:15460; CACNA2D3.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 2.
DR Pfam; PF00092; VWA; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50234; VWFA; 1.
SQ SEQUENCE 997 AA; 112996 MW; B56D13133FD67B8D CRC64;

Query Match 56.8%; Score 3250.5; DB 2; Length 997;
Best Local Similarity 60.5%; Pred. No. 1.3e-188;
Matches 593; Conservative 177; Mismatches 191; Indels 19; Gaps 6;

QY 66 MENMLRKRKVAQNVLVEAAEEADLNHEFNESLVFDYVNSVLINERDEKGNFVGLGAEFL 125
DB 1 MEEMFHKKSVAARLVRAEAAHLKHEFDADLQYEFNAVLIINERDKGNFLELGKEFIL 60

QY 126 ESNAHFSNLPVNTSISVQLPTNVYKDPDILANGVYMSEALNAVVFENFORDPTLTWQYF 185
DB 61 APNDHFNNLPVNLSDVQVPTNMYNKDPALVNGVYWSLNVKVFVDNFDPRDPSLIWQYF 120

QY 186 GSATGPRRIYPGIKWTDPDENGVIITFDCNRNGWVIOAATSPKDIVILVDVSGSKMLRMTI 245
DB 121 GSAKGFPQPGIKWEPDENGVIITFDCNRNRKWIQAATSPKDVVILVDVSGSKMLRLTI 180

QY 246 AKHTITITLDTGENDPVNIIAYNDVYHYTEPCFGLVQADRNREHFKLLVEELMVKG 305
DB 181 AKQTVSSILDTGDDDFNIIAYNEELHYVEPCUNGTLVQADRTNKEHFEHLDKLFAKG 240

QY 306 VGVVDQALREAFQILKQFQBAKQGLSCNQAIMLISDGAEDYBPFVEKYNWPPCKVRVFT 365
DB 241 IGLMDIALNEAFNLSDFNHTGQSGICSAQIMLITDGAVDYDTIFAKYNWPPCKVRIFT 300

QY 366 YLIGREVSFADRMKWIACNNKGYTQISTLADTQENVMYHLVLSRPMVINHDHDIWTE 425
DB 301 YLIGREAAFDNLKWMACANKGFFQTISTLADYQENVMYHLVLSRPMKVIDQEHVDVWTE 360

QY 426 AYWDKSLSSQAOSLT-----LLTTVAMPVFSKQNETSRSHGILLGVVGSDDVALRELMLK 479
DB 361 AYIDSTL--PQAQLTDQDQPVLTMTVAMPVFSKQNETSRSHGILLGVVGTVDVPKELLKT 418

QY 480 APRYKLGHVGYAFINTNNGYILSHPLDRLPYREGKKLKPKNYNSVDLSVEVEDQAESL 539
DB 419 IPKYKLGIGHGYAFATNNGYILTHPELRLLYEKGK-RRKPNYSSVDLSVEVEDRDDVL 477

QY 540 RTAMINRETGTLSDNVKVPMDKGRVFLFNTDFFFTDIDTPFSLGALVSRGHGEVILLG 599
DB 478 RNAMVNRKTKFSNEVKTKYDVKGRVLVMTNDYYTIDIKGTFPSLGLVLSRGHGKFFRG 537

QY 600 NTSVEGLHLLPDLALAGDWYTCITIDIDPHRKLSOLEAMIRFTRKPDLECEDELV 659
DB 538 NVTIEGLHLDHPDVSADENSYCNVDLHPEHRHLSQLEAIKLYLKGKPEPLQCDKELI 597

QY 660 REVLFDVAVTAPMEAYWTALALNNSESEHVDMAFLGTGTRALLRSLFVSGSEKVSORKF 719
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Db 598 QEVLFDAVVSAPIEAYWTSIALNKSNSDKGVEVAFGLTRTGLSRINLFVGAELTNQDF 657
QY 720 LTPEDASVFTLDRFPLWTRQASEHPAGSVFNLRAEGBESAGEPMVWTASTAVATVD 779
Db 658 LKAGDKENIFNADHPLWYRAAEQIPGSFVYISFTSGP--VNKSNVVTASTSIQLLDE 715
QY 780 KRTAIAAAGVOMKLEFLQRKFWAATROCSCTVDGPTVQSCEDSDLDLCFVDDNNGFILISK 839
Db 716 RKSPVVAAGVIOQMKLEFFQRKFWTASROCASLQKCSISCDDETVCYLIDNNGFILVSE 775
QY 840 RSRETGRFLGEVDGAVLTOLLMSGVFSQVTMYDQAMCKPSSHHSAAQPLVSPISAFLT 899
Db 776 DYTQTGDFGFEIEGAVNMKLLTWGSKFRITLYDQAMCRANKESSDGAHGLDPPYNAFLS 835
QY 900 ATRWLLQELVLFLLEWSVWGSDYDRGAEAKSVFHHSHKHKQDPLQPCDTEYFVYVQPA 959
Db 836 AVKMIWTELVLFVFNLC--SMWHSMTAKA-----QKLKOTLEPCDTEYPAFVVSERT 887
QY 960 IREANGIVECGPCQKVFVVOQIIPNSNLLLVTDPTCDCSIFPPVLQEADEVKYNASVKCD 1019
Db 888 IKETTGNIAECDCSKSFVIOQIIPSSNLFMWVVDSSCLCESVAPITMAPIIRYNESLKCE 947
QY 1020 RMRSQKLRRRPSCHAFHPE 1039
Db 948 RLKAQKIRRRPESCHGFHPE 967

RESULT 8
Q9NY18 PRELIMINARY; PRT; 519 AA.
AC Q9NY18;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Calcium channel alpha2-delta3 subunit.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=21142395; PubMed=11245980; DOI=10.1016/S0378-1119(00)00600-4;
RA Hanke S., Bugert P., Chudek J., Kovacs G.;
RT "Cloning a calcium channel alpha2delta-3 subunit gene from a putative
RT tumor suppressor gene region at chromosome 3p21.1 in conventional
RT renal cell carcinoma.";
RL Gene 264:69-75(2001).
DR EMBL; AJ272213; CAB75878.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 1.
DR Pfam; PF00092; VWA; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50234; VWFA; 1.
SQ SEQUENCE 519 AA; 59526 MW; 198D13AF246286C6 CRC64;

Query Match 32.6%; Score 1866.5; DB 2; Length 519;
Best Local Similarity 68.9%; Pred. No. 6.1e-105;
Matches 344; Conservative 71; Mismatches 81; Indels 3; Gaps 2;

QY 66 MENMLRKRKVAQNVLVEAAEEADLNHEFNESLVFDYVNSVLINERDEKGNFVGLGAEFL 125
DB 1 MEEMFHKKSVAARLVRAEAAHLKHEFDADLQYEFNAVLIINERDKGNFLELGKEFIL 60

QY 126 ESNAHFSNLPVNTSISVQLPTNVYKDPDILANGVYMSEALNAVVFENFORDPTLTWQYF 185
DB 61 APNDHFNNLPVNLSDVQVPTNMYNKDPALVNGVYWSLNVKVFVDNFDPRDPSLIWQYF 120

QY 186 GSATGPRRIYPGIKWTDPDENGVIITFDCNRNGWVIOAATSPKDIVILVDVSGSKMLRMTI 245
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Db 121 GSAKFFRQVPGIKWEPDENGVIAFDRCNRKRWYIQAATSPKVVVLVDVSGSKMGLRLTI 180

Qy 246 AKHTITTLTDLGENDFNIIAYNDYVHYIEPCFKGILVQADRNRRHFLLVBEELMVKG 305

Db 181 AKQTVSSILDTLGGDDFFNIIAYNEELHYVPCPLNGTLVQADRNKHFREHLDKLFAKG 240

Qy 306 VGVVDQALREAFQILKQFOEAKQSGSLNQAIIMLISDGAVEDYEPVPKYNWPDCKVRVPT 365

Db 241 IGMULDIALNEAFNLISDFNHTGQSGISQAIIMLITDGAVDYDTIFAKYNWPDCKVRIFT 300

Qy 366 YLIGREVSFADRMKWIACNNKGYTQISTLADTQENWVYHLVLSRPMWLNHHDHDIWTE 425

Db 301 YLIGREAFADNLKWMACANKGFTQISTLADVOENWVYHLVLSRPMVLDQEHVDVWTE 360

Qy 426 AYMDSKLLSSQAQSLTLLTIVAMPVFSKQNETRSHGILLGVGSDVALRLMKLAPRYKL 485

Db 361 AYIDSTLTDQGP--VLMTTVAMPVFSKQNETRSGILLGVGTDVDPVKELLTIPRYKL 418

Qy 486 GVHGYAFINTNGVILSHPDRLPIYREGKLLKPKPNTNSVDLSEVEWEDQASLRITAMIN 545

Db 419 GIHGYAFATITNGVILTHPELRLLYEKGK-RRKPNYSYVDLSEVEWEDRDDVLRNAMVN 477

Qy 546 RETGTLSDMVKVPMDKGR 564

Db 478 RKTGKFSMEVKKTVDKGR 496

RESULT 9

Q9V6T7 PRELIMINARY; PRT; 1218 AA.

AC Q9V6T7; Q8T9C3;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE CG1295-PB (SD07723p).

GN ORFNames-CG12295;

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20196006; PubMed=107311132; DOI=10.1126/science.287.5461.2185;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Anandides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.P.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brannon R.C., Rogers Y.H., Blazer R.G., Champagne M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,

RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolehakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Buam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke A., Davenport L.B., Davies P.,

RA DePablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Foaier C., Gabriellian A.C., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Minkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,

RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J.,

RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195(2000).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426065; PubMed=12537568;

RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,

RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,

RA Pacleb J.M., Park S., Pfeiffer B.D., Richardson S., Sodergren E.J.,

RA Svirkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,

RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila

RT melanogaster euchromatic genome sequence.";

RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426070; PubMed=12537573;

RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirkas R.,

RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,

RA Ashburner M., Celniker S.E.;

RT "The transposable elements of the Drosophila melanogaster euchromatin:

RT a genomics perspective.";

RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426069; PubMed=12537572;

RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,

RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.;

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

RT systematic review.";

RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RN [5]

RP SEQUENCE FROM N.A.

RX FlyBase;

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

RN [6]

RP SEQUENCE FROM N.A.

RX FlyBase;

RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

RN [7]

RP SEQUENCE FROM N.A.

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,

RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,

RA Miranda A., Mungall C.J., Nunoo C., Pacleb J., Paragas V., Park S.,

RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,

RA Celniker S.;

RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; A5003817; AAF58335.2; -;

DR EMBL; AY069830; AAL39975.1; -;

DR FlyBase; FBgn0033870; CG12295.

DR GO; GO:0016020; C:membrane; IEA.

DR InterPro; IPR004010; Cache.

DR InterPro; IPR002035; VWF_A.

DR Pfam; PF02743; Cache; 2.

DR Pfam; PF00092; VWA; 1.

DR SMART; SM00327; VWA; 1.

DR PROSITE; PS0234; VWFA; 1.

SQ SEQUENCE 1218 AA; 140048 MW; 4F04224063D527B5 CRC64;

Query Match

27.1%; Score 1551; DB 2; Length 1218;

Best Local Similarity 33.0%; Pred. No. 3.2e+85;		Matches 397; Conservative 207; Mismatches 365; Indels 234; Gaps 43;	
Qy	13	VKLWADTFGGDLNTVNTKYSGSLLLOKYYKDVSSLKIEV---DGLYLVKRSSEDMNM	69
Db	40	VHSWADKGLMELF-----HLGDFITRR--KEVQESFKDAKAVSRNGASIVDSMAKETEMM	92
Qy	70	LRRKVEAQVQLVFAAEADLNHEFN-BSLVFDYVNSVLINERDEKGNFV-----	117
Db	93	MDLKVSARIMDTAENTALSQNDMADKMFYSYA---KEMLEPGDPVPPIPTAPDMD	149
Qy	118	-ELGAEL-----LESNAHFSNLPVNTSISVOLPTNVYKNKDDPLNGVYMSEALNA	168
Db	150	KDIGEPLIYQPKVVVLEPRPEFHNTPVNFSVSVHVPVNVFDRAPDVIKAIQWSENLDQ	209
Qy	169	VFVENFORDTLTWQYFGSATGFPRIYPGIKWTPDENGVITFDNRNGWTIQATSPKDI	228
Db	210	IFRDYKNDPTLSQWFGSGTSFGMRQFPASKWRKDV--PVDLYDCLRLSWTMEATSPKI	268
Qy	229	VILVDVSGSMKGLRMTIAKHTITITLDTLGENDFVNIAYNDVYHYIEPCFKGILVQADR	288
Db	269	VILMDGSGMLGQELDIKXHVNTILDTLGTNDFVNIFTFDKEVSPVPFCFETLQANL	328
Qy	289	DNREHFLLVVELVMVGVGVDQALREAFQILKQFOBAKQSGSLCNQAIMLISDGAEDYE	348
Db	329	GNIRELKEGIELPRKSIANYTAALTAKAFELLEETKLSRGAQCNOAIMIIGDAPENNR	388
Qy	349	PVEKYNW---PCKVRVFTYLGREVSFADRMKWTACNKGYYTQISTLATDQENMEY	405
Db	389	EVFELHNWRDPYKPRVFTYLGKEVANWDDIRWMACENQGYVHLSDTAEVREVMVNY	448
Qy	406	LHVLRRPMVI-NHDHDIIMTEAYMD-----	434
Db	449	IPWAPLVLGRDHPVINSQVADIEDTKLSYLDINDICEYQKADVLEYQVHDMLE	508
Qy	435	S-----QAQSLTLTTTAMPVFSKQNETRSHGILLGVGSDVALRE	475
Db	509	PSEHRRKYRMRKETNQPVDSNVYQPMTVSPPIVDRRENATRIANILVAGTDVPINE	568
Qy	476	LMKLAPYKLGVGHYAFLNTNGVILSHDPLRYREGKLLKPKPNVNSVDLSEVEDQ	535
Db	569	IKLLGFTLVNGVYAFIVTNGVLFPHDPFRPIF-QGYILKFA--YNSVDMLEVELLDD	625
Qy	536	AE-----SIRUTAMINRETGTLSDMKVPMDKGRVLTFTNDYFFDDISDTPFSLG	585
Db	626	DRAPDNFVLMTIROSIINQSGSKWMLVKNHFDKMRVARVKRYQYWTAIKKTFTLV	685
Qy	586	AVLSRGHG-----EYILLGNT---SVEEGLHDLHLPLDALAGMIYCIITDIDP	630
Db	686	ISYPEQYGVSHMDIRADQETHRISIKGTNLSRVFSGRWKIHP-----DWLFC-----	733
Qy	631	DHR-----KLSQLEAMIRPLTRKD-----PD-----LECDLELVRELVDAVY	668
Db	734	KHSNRTFKTPEIE-LYLFELRMSEPGMRWPGSSAMPPEHAAAMFCDRQLMQALVFDARV	792
Qy	669	TAPMEAYWTA--LALANSESEHV-----VDMAFGLTRAGLRLSSLF---VSGSEKVSDR	717
Db	793	TG-----WFSNNTSFNSKDKNGEFKQRFQVTVAFATHSGLTRMHEFHSNAAEESGVGE	847
Qy	718	KFTUTPEDEASVFTLDRPPLWYQA-SH--PAGSFVFNLRWAGSPSAGE---PMVVTAS	771
Db	848	TF-----SQNNTRAIDE--IWYKRAVDQHFVREESFVYSV-----PFDAGSSNEILVTAS	896
Qy	772	TAVAVTVDBETATAAAGVQMKLEFLQRFKFWAATRCQSTVDGPTYQSCEDSDLDGCFVION	831
Db	897	HAVFHNEGKTAFAAVVGFQFQSHALYKLFPHNITGNACAVD-----DKDCYILDN	946
Qy	832	NGFILSKRSRETGRFLGVDGAVLTQLLSGMVFSQVMTYDYQAMCKPSSHHSAAQPLV	891
Db	947	NGVVIISTRVHETGRFPFGEVNGAIMKLELLENVYRVQTVYDQAVCFESKNDNNASSMLL	1006
Qy	892	SPISAFLTATRWLLQELVLF---LLEWS--VWGSWTDRGAEKSV-----FHHSHK	937

Db	1007	SPLFHLRLRVGKWLHTALWYIVQLQWAPGVSSHYADMYGDSNDTEPPPPHPHDHARN	1066
Qy	938	---HKQDP-----LQPCDTEYVPVYQPAIREANGIV---ECGQCQKVYV	978
Db	1067	GNHGKGDHDDHWLRYTLHRTLKPCDKMRDLTY--LNFNEKDNVYVNTMTAHACERPFV	1123
Qy	979	QQIPNSNLLLLVTDPTC--DCSIFFPVLOEATE--VKYNASVKCDRMRSOKLRRRPPDSCH	1034
Db	1124	LPFPNSNLLLLVTDQCPDGSVVLTWNPQIDYHLSVNDSLACYKQAREFNMRPHSCI	1183
Qy	1035	AFH 1037	
Db	1184	SRH 1186	
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DT	01-MAR-2003 (TEMBLrel. 23, Last sequence update)		
DT	01-MAR-2004 (TEMBLrel. 26, Last annotation update)		
DE	CG12455-PB.		
GN	ORFNames=CG12455;		
OS	Drosophila melanogaster (fruit fly)?		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7227;		
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RA	Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RA	Amanatides P.G., Scherz S.E., Li P.W., Hoskins R.A., Galle R.F.,		
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,		
RA	Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,		
RA	Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,		
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,		
RA	Abriel J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,		
RA	Balaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,		
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,		
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,		
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,		
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RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,		
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,		
RA	Foster C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,		
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,		
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,		
RA	Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,		
RA	Talali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,		
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,		
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,		
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,		
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,		
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,		
RA	Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,		
RA	Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,		
RA	Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,		
RA	Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,		
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,		
RA	Swirekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,		
RA	Wang Z.Y., Wasarman D.A., Weinstein G.M., Weissenbach J.,		
RA	Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,		
RA	Yeh R.F., Zaveri J.S., Zhan M., Zhang Q., Zhao Q., Zheng L.,		
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,		
RT	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;		
RL	"The genome sequence of Drosophila melanogaster.";		
RN	Science 287:2185-2195(2000).		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=22426065; PubMed=12537568;		

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OX Eohydroidea; Drosophilidae; Drosophila.
RN NCBI_TaxID=7227;
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RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
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RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheier F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodgett J., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN [2]
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RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426072; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradscky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [7]
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RC STRAIN=Berkely;
RX MEDLINE=99403001; PubMed=10471707;
RA Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
RA Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
RA Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
RA Palazzolo M., Reese M.G., Spradling A., Teang G., Wan K., Whitelaw K.,
RA Celniker S., Rubin G.M.;
RT "An exploration of the sequence of a 2.9-Mb region of the genome of
RT *Drosophila melanogaster*: the Adh region.";
RL Genetics 153:179-219(1999).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RA Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
RA Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
RA Farnon D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
RA Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
RA Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
RA Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
RA Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
RA Zieran L.L., Rubin G.M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
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DR ENBL; AB003650; AAF53505.2; -;
DR ENBL; AB003415; AAF4988.1; -;
DR FlyBase; Fggn0028859; CGI2455.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 1.
DR Pfam; PF00092; VWA; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS0234; VWFA; 1.
KW Hypothetical protein.
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Query Match 25.2%; Score 1441; DB 2; Length 2190;
Best Local Similarity 32.3%; Pred. No. 3.7e-78;
Matches 378; Conservative 187; Mismatches 373; Indels 234; Gaps 44;
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DB 20 WATQFGDELPAQAQKTKSQEIKYK--EYNARVELKNGTELKTSITKNVGRMLARKMD 77
QY 76 AVQNLVEAAEADLNHEFNESLV---FDYNSVLI----NERDE----KGNFVELGAFL 124
DB 78 AVRCIQERAEYVNEFENFNLTVQALQFTYFSSKYSTFNNGSSELEPNEAEFAWMYRNME 137
QY 125 LESNAFNSLNPVNTSSVOLPTNVNKPDPDILGVYMSALNAVVFENFQDPDTLTWOY 184
DB 138 LNPDTHTFYNTPDVTEHSSVHVPSNIWDRSERVLKTMWSEHLDEVFRQNTQSPALSWQY 197
QY 185 FGSATGFFRIYPIGKIWT---PDENGVIITFCNRRGWYIQAATSPKDIIVLVDSGSMKGL 241
DB 198 FGSDTGLRHYPAAQWTDTRPNRDDADTYDCRKSWEYIETATCSKDIIVLLDHSGSGMTGF 257
QY 242 RMTIAGHTTTTLDTGTGENDFNVIAYNDVHYIECFKGLIVQADRDNRHEFKLLVEEL 301
DB 258 RHHVAKFTIRSLDFTSNNDFFTLIRYSSEVNDIIFCPNGALVQATPENIEVFNQIQIEQL 317

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Qy 357 -----PDCKVRVFTYLGREVSFADRMKWTACNKGYYTOISTLAQTQENVMYLVLS 410
Dy 378 NGENGTQMDTRVFTYLGKEVTKREIQOMACLNRGYSHVQVLDHEVHEVLKYVDVIA 437
Qy 411 RPMVI-NHDDIHWTEAYMDSKL---LSSQAQSLTLTTVAMPVFSK-----KNETRSHGIL 463
Dy 438 TPLVLQNEHQPTWTHAFTDXTYDPTKSNEKRPRLMISGVGPAFDRFVRHANSTNPRARL 497
Qy 464 LGVVGSDVALBELMKLAPRYKLGHGVAFLTNNGYILSHPDRLPLVREGKKLKPKNYN 523
Dy 498 LGVAGTDPVEDIDIKLTPYKLGNGYSFVSNNGYVLLHPDLRPIGTNGKM---NPNYN 554
Qy 524 SVDLSEVE--WEDQA-----ES---LRTAMNRETGTIL-SMDVKVPMDKGRVLFNTDY 572
Dy 555 SIDTVEVHLFEDQSPREPESILHIRNVMVRHEANFEKLSVFKHYDKMRVSEEKQDY 614
Qy 573 FTFDISDTPFSLGAVLSRGHGE-YILLG-----NTSVEEGLHDL-----LHPDLALAG 619
Dy 615 FFAPLNTPTFLGIVMPSEYKGTWKVGEVVDKXHKMKINISDFFIGENMKVHP----- 668
Qy 620 DWIYCIITDIDPDHKKLSOLEAMIR-FLTRKDDPLE-----KDDKDLNCGRKTL 727
Dy 669 DWYVCKHYLEGH-EFKTPEAELREFLAKMNDKWKSEQVAEDSDWDDKDDKDLNCGRKTL 727
Qy 654 -----CDEELRVFLDPAVVTAPMEAYWTALANMSESEHV-----VDMFLGTRAGLL 703
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Qy 704 RSSLFVGESEKV-SDRKF-----LTPDEASVFTLDRFPLWYRQA-----SEHPAGSFVFNLR 754
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AC Q70758;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE AGCP5954 (TrEMBLrel. 26, Last annotation update)
GN Name=agCG56326; ORFNames=ENSANGG0000018729;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008960; EAA10906.1; -.
DR GO; GO:0016020; C-membrane; IEA.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 1.
DR Pfam; PF00092; VWA; 1.
DR PROSITE; PS0234; VWA; 1.
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Query Match 25.0%; Score 1430.5; DB 2; Length 1028;
Best Local Similarity 33.1%; Pred. No. 5.2e-78;
Matches 349; Conservative 181; Mismatches 333; Indels 191; Gaps 29;
Qy 13 VKLWADTFGGDLVNTVTKYSGSLLQLKKYKDVSSSLKIEV---DGLLEVRKPSSEDMNM 69
Dy 4 VQAWAAKLGGLW-----HLGDFITRR--KEVESFKQAQVVMKNGAKIIVEAKDLKYM 56
Qy 70 LRREKAVQNLVEAAEADLNHEFNSLV---FDYNSVLINERDEKGNFVEL----- 119
Dy 57 MDAKVSARKIMTDAENTAIS--FDEPVNQSFQYNA---KOMIEPEIITTPIMIDE 111
Qy 120 -----GABFLLESNAHFNLPVNTSISSVQLPTNVNKPDPDILNGVYMSEALNAV 169
Dy 112 DPADITTPPKGIIVLTKKRHFNEAVNTTVSSVHVPTNVYDRATEVIAKHKSEALDSI 171
Qy 170 FVENFORDPTLTWQYFGSATGFPRIYPIGKIWTDPENGVIITFDCNRNGWYTOATSPKDIV 229
Dy 172 FYNNYIGDPTLTWQYFGSSGFLRPFPATKW--EQDPVDLYDCRLRSWYIEAANSKMDL 229
Qy 230 ILVDVSGSMKGLRMTAKHTITITLTGLGDNFVNIAYNDYVHYIEPCFKILVQADRD 289
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Dy 290 NIRELKGMDNIETNEIANVSAALTRAFELLEQFRETNGARCNCQAIMLVSDGVPSFDE 349
Qy 350 VFEKYNW---PDCKVRVFTYLGREVSFADRMKWTACNKGYYTOISTLAQTQENVMYEL 406
Dy 350 VFEQFNWKELPFTPVRFVFTYLGREVADVKEIKEMACRNGQYVYVHLSTMAEVRREVLNYI 409
Qy 407 HVLSRPMVNL-HDHDIIWTEAYND-----SKLL----- 433
Dy 410 PVITARPLVLNKRHPVMSIYADVDDPKMTDLWEIKERAOKERPIDVRKRVLYSP 469
Qy 434 -----SSQAQSLTLTTVAMPVFSKQNETRSHGILLVGVSDVALREL 476
Dy 470 EEOHRRWIMKQRMNQDPYSNTQKYNFMTTVSVFDRRENATRVANILGVAGADVPAEI 529
Qy 477 MKLAPRYKLGHGVAFLTNNGYILSHPDRLPLVREGKKLKPKNYNVDLSEVED-- 534
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Qy 764 EPMVVTASTAVAVTVDKRTAIAAAGVQMKLEFLQRKFMAATRCQSTVDGPTQSCEDSD 823
Db 867 NDTLVTASHAIFHADGAREAPVAVGQFPHHSALYTLFKNITSQCGHGDPRCEKTCFTGD 926
Qy 824 LDCFVDNNGFLLSKRSRETGRPLRGVDAVLQTLLSMGVQSVQVNTYIDYQAMCKSPSHH 883
Db 927 YQCVVIDNNGFVWISQLOQETGAFFGVEKPAFMQRLDDSIERNVTYDYQAVCFMAKGS 986
Qy 884 HSAAQPLVSPISAFLTATRLMLQELVLFLEWSV 917
Db 987 INLGTVLQTP-----LRLLMWLLNTFTSYLV-WVV 1015

RESULT 13
Q7PM00
ID Q7PM00 PRELIMINARY; PRT; 1011 AA.
AC Q7PM00;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000020925 (Fragment).
GN Name=ENSANGSG0000018436;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anophelinae.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR ENBL; AAB01008980; EAA14572.2; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 1..
DR Pfam; PF00092; VWA; 1..
DR PROSITE; PS0234; VWFA; 1.
FT NON_TER 1011 1011
SQ SEQUENCE 1011 AA; 117662 MW; 70C7D6B71CC93E59 CRC64;

Query Match 24.4%; Score 1398; DB 2; Length 1011;
Best Local Similarity 33.2%; Pred. No. 4.8e-76;
Matches 340; Conservative 184; Mismatches 351; Indels 150; Gaps 32;

Qy 16 WADTFGGDLVNTYKYSGLLQKKYKDVSSLIKIEVDGLVLRKFSEDMENMLRRKYE 75
Db 4 WADNFGELWDLAQTTKAMEITAKYKAYNA--RVEHKDGTALIQSIVENVRGMRFKMD 61
Qy 76 AVQNLVEAAEADLNHEFNSLV--FDYNSVLIN-----ERDEKGNFVE---LGAEFLL 125
Db 62 AIKCIINLAEELSEQEPEFNETLADNFYSYSSKYSNIDGRPEPIPETLQENMMMYRMSL 121
Qy 126 ESNAHFSNLPVNTSISVOLPTVYVYKNDPDLNGVYMSALNAVVFENFORDPTLTWQYF 185
Db 122 NPTHEFNISVNTSYSVHVPQVNDYRPVWLEALQWSLDDVFLQVNSDPAWSQYF 181
Qy 186 GSATGFFRIYPGIKWTPDENGVITFCRNRGWYQAATSPKQIVILVDVSGSMKGLRMTI 245
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Db 182 GSYTGLMRHPALEWNRH--VDTFCRKESWIETATCSKQIVILLDNSGSGMTGYRNYI 239
Qy 246 AKHTITITLDTLGENDFVNIANDVHYHIEPCFK-----GI 282
Db 240 AQLTVKSIILDTFNNDFINIYKYSNDVEPLVPCFKVGLKILDEKCNRVRFNNTSLIQDM 299
Qy 283 LQADRDNRHHPKLLVEELMVKGVVVDQALREAFQILKQFOEAKQ---GSLCNOAIML 338
Db 300 LVQATPENMRFFNEYRELLPEGYANVKAFVAAFELLQYREIRRCNBSVSGCNQAIML 359
Qy 339 ISGAVEDYEPVEPEKYNW----PDCKVRVFTYLIGREVSFADRMKIACNKGYYTOIST 394
Db 360 ITDGVPSNITEVEFAYNWFENGTKIPVRVFTYLLGREVTKVREIQMACLNRGYSHIQS 419
Qy 395 LADQENWMEYLHLSRPMVINH-DHDIITWEAYMDS--KLL--SSQAQSLTLTTVTAMP 449
Db 420 LDEVOEVLKYYVTIATPLVQGVHEPPTWHTAFTDAENLLTEADDDPEPRLMIAVGAP 479
Qy 450 VFSKK---NETRSHGILLGVGSDVALRELKMLAPRYKLGHVHGYAFLNTNNGVILSHPD 505
Db 480 AFDKKNHYNETRT--ARLLQVAGTDIPVEDLDELTPYKLGVNGYSFIVSNGGVLMHPD 538
Qy 506 LRPLYREGKLLKPKPNYNSVDLSEVW-----EDQAE-----SLRTAMINRE 547
Db 539 LRPV-----SNGRLKENYSIDLTEIEQIYDENITROIEDMTGREMSPFILELRQLHVDQS 594
Qy 548 TGTLS-MDKVPMDKGRVLFNTDYFFTDISDTPFSLGAVLSRGHGE-YILG-----N 600
Db 595 FGNMTKLPVRPHYDKMRRVSLQYQYVYAPLENTPEFSLGLVLPDHYGSTMVKGDEIKRN 654
Qy 601 TSVEEGLHDL-----LHPDLALAGDWLYCITDIDPDHRLKLSQLEAMIRFLTR----- 647
Db 655 QHMLNISDFFMGDNWKVHP-----DWYCKHYLEGHEFTKPTPELHRHFLNRLYEPTW 708
Qy 648 -----KDPDLECEDELVREVLFDVAVVTAPMEAYWTALALN 682
Db 709 KWSQQVEPEPNKESDGPNGRKRTLDDDAYCNKELVQLLIPDAKVTNNSYRNWEF---- 764
Qy 683 MSESEHVVDM-----AFLGTRAGLRSSLFVGVSEKV-SDRKFLTPEDEASVTLDRFPL 736
Db 765 ENENERKIIEMYNATLRFVATMSGLTRWQFI FGEVEVDTDSDFGYHKKK-----IDE--T 818
Qy 737 WYRQA--SEHPAG--SPVFNLRWAEGPSAGEPMVVTASTAVAVTVDKRTAIAAAGVQMK 793
Db 819 WYRSAILQHKIDPKSFVSVPHESDPEDGE-LKVTAATWAIIPRDGGLAEPGCVTGQFT 877
Qy 794 LEFLQRKFWAATRCQSTVDGPTQSCEDSDLCDFVDNNGFLLSKRSRETGRFLGEVDG 853
Db 878 HSLMYDRFMEITSK-TTCDG-CIETCASESRDCYVIDHNGVYVLSNHTGFRFFGEIEG 935
Qy 854 AVLTQLLSMGVFSQVMTYDYQAMCKPSSHHHSAQAQPLVSPISAFLTATRLMLQELVFL 913
Db 936 AIMQSMVDKEIFTMTITVFDLQGLCEYERVVENDATALLHPMKVFMGLGLKLTAEIAML 995
Qy 914 EWSVW 918
Db 996 RFDWF 1000

RESULT 14
Q9NK83
ID Q9NK83 PRELIMINARY; PRT; 1255 AA.
AC Q9NK83;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein BG:DS07108.2.
GN Name=BG:DS07108.2; ORFNames=CG4587;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
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OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=99403001; PubMed=10471707;
RA Ashburner M., Miera S., Rote J., Lewis S.E., Blazej R., Davis T.,
RA Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
RA Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
RA Palazzolo M., Reese M.G., Spradling A., Teang G., Wan K., Whitelaw K.,
RA Celnikier S., Rubin G.M.;
RT "An exploration of the sequence of a 2.9-Mb region of the genome of
RT Drosophila melanogaster: the Adh region.";
RL Genetics 153:179-219(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Celnikier S.E., Agbayani A., Arcalana T.T., Baxter E., Blazej R.G.,
RA Butenoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
RA Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
RA Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
RA Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
RA Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
RA Sethi H., Snir E., Svirskaas R.R., Wan K.H., Weinburg T., Zhang R.,
RA Zieran L.L., Rubin G.M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003413; AAP44957.1; -
DR FlyBase; FBgn0028663; CG4587.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF02743; Cache; 1.
DR Pfam; PF00092; VWA; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS00234; VWFA; 1.
KW Hypothetical protein.
SQ SEQUENCE 1255 AA; 140745 MW; FEB584D76C7785C6 CRC64;

Query Match      22.8%; Score 1305.5; DB 2; Length 1255;
Best Local Similarity 29.1%; Pred. No. 2.8e-70;
Matches 328; Conservative 203; Mismatches 403; Indels 195; Gaps 30;

QY 80 LVEAAEADLNHPENSLV-----FDYNSVLINERDEKGNFVELGAEFLLESNAHFSN 133
DB 116 LMSAEQAALSELEGGQQAESPMGGQOQHYDARRINEYNADGKLADGARHMDIRFMRFR 175

QY 134 LPVNTSSVOLPTNVNKKDPIILGVYMEALNAVVENFORDPILTMQYFGSATGFFR 193
DB 176 LPVNLSSILVPGVDLDEPDVKSALQWSGHLDPLEQNLEQDPALSWQYFGSGTFLR 235

QY 194 IYPIGIKTPD--ENGVTTPDCNRNGWYQIATSPKDIIVLVDSGSMKGLRMTIAKHTIT 251
DB 236 RFPCTAMPPEGSKGLIHDFRTHNFWFQAASSPKDIMILLDASSSMTEKSFOLGMATAF 295

QY 252 TILDTLGENDFVNIANDYVHYIEPCFKILVQADRDNRHFKLLVLELWVGVGVDQ 311
DB 296 NILDTLGEDDFVNLITFEVVVTKTPVPCFKORMVRATPDNTQETKSAVKAIKLQDNTANFTA 355

QY 312 ALREAFOILQFOBAKQSGSLCNOAILMISGAVDYEVPFEKYNWPCVKRVFTYILIGRE 371
DB 356 GLEYAFELLLKYNQSGAGSQCNQAILMITESTSESHKQVVKQYNWPHMPVRIFTYILIGSD 415

QY 372 VSFADRMKVIACNNKGYTQISTLADTQENVMYELHVLSPMWI-NHDDHIITWEAYMDS 430
DB 416 SGSRSLNLDHMACSKNGFFVQINDYDEARRKVIDYALVMARPMIMYQADHPVHNSPVFVAG 475

QY 431 K---LLSSQAQSLTLTTVAMPVSKQNETRSHGILLGVGSDVALBELMKLAPRYKLG 487
DB 476 KSGGLGRDSEYQRRLVTTVTPVDFDRNHSVRVANLLGVGVDVPIBEIRKVPQHKLGP 535

QY 488 HGVAFLTNNGYILSHLDPLRYREGKLL-KPKPNYNSVDLSEVW----- 532
DB 536 NGYSFIVDNGRVLHPDLPLDGLDQNGYIDQLKPKYASVDITELPLETFEFGNNEPIEI 595
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Db      892  A W L S L M P A S L R A W P Q E S Y T Y D N E D V F V D N N Y S D E Y E F G N E N E Y N M Q V D Q E M D E F F T T A D 951
Qy      928  A K S V F H H S H K H K - - - - - K Q D P - - L Q P C D T E Y P V F V Y Q P A I R E A N G - - - - - I V E C - 969
Db      952  V E Y T P P P R Q H K P H V G P R F S P D P H N A R C D L R T D L Y M L Q P E R L N Q G G O N N P L K G K L T N C H 1011
Qy      970  - G P C Q K V F V Q Q I P N S N L L L V T D P T C D C - - - - - S I F P P V L Q E A T E Y K Y N A S V K C D R M R - 1022
Db      1012 V S G C E R P F S V Q K I P H S N L L I L L V D T L C P C G S K Q L D I E P - - L E E A G V I G - - - - - A C S T R R Q 1064
Qy      1023 - - S Q K L R R R P D S C H A F H P E 1039
Db      1065 G Q E O E S R R R P K K C I N Y H P E 1083
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Search completed: November 16, 2005, 03:22:51
Job time : 196 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 16, 2005, 19:23:23 ; Search time 1314 Seconds

(without alignments)
4910.592 Million cell updates/sec

Title: US-09-833-222A-10

Perfect score: 5726

Sequence: 1 MAVALGTRRRDRYKVLWADTF.....MPMPTPVPVLGGNIRYAL 1090

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US09833222/runat_15112005_145357_15779/app_query_fasta_1.1287
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-UNITS=bites -START=1 -END=1 -WATRI-X-blosum62 -TRANS=human40.cdi -LIST=45
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-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: Geneseq16Dec04.*
- 2: Geneseq1980s.*
- 3: Geneseq1990s.*
- 4: Geneseq2000s.*
- 5: Geneseq2001as.*
- 6: Geneseq2002as.*
- 7: Geneseq2002bs.*
- 8: Geneseq2003as.*
- 9: Geneseq2003bs.*
- 10: Geneseq2003cs.*
- 11: Geneseq2003ds.*
- 12: Geneseq2004as.*
- 13: Geneseq2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5726	100.0	3486	10 ADF71819	Adf71819 Human cal
2	5726	100.0	3486	10 ABZ20598	Abz20598 Human vol
3	5386.5	94.1	5073	3 AAA09254	Aaa09254 Human alp
4	5385.5	94.1	4841	10 ADE07110	Ade07110 Novel cod
5	5342.5	93.3	3339	4 AAS01433	Aas01433 Human sec

6	5342.5	93.3	3339	5 AAF57570	Aaf57570 Human cal
7	5276	92.1	3209	4 AAS01432	Aas01432 Human sec
8	5276	92.1	3209	5 AAF57569	Aaf57569 Human cal
9	5234.5	91.4	3228	6 AAS17581	Aas17581 DNA encod
10	5230.5	91.3	3345	6 AAS17582	Aas17582 DNA encod
11	5197.5	90.8	5713	3 AAA09278	Aaa09278 Human alp
12	5148	89.9	3201	4 AAS01431	Aas01431 Human sec
13	5148	89.9	3201	5 AAF57568	Aaf57568 Human cal
14	5127.5	89.5	3742	13 ADN33188	Adn33188 Human tra
15	3808	66.5	4125	6 AAD22004	Aad22004 Human tra
16	3416.5	59.7	3690	6 AAD26399	Aad26399 Human cal
17	3410.5	59.6	3770	3 AAA09253	Aaa09253 Human alp
18	3410.5	59.6	3770	4 AAS01414	Aas01414 Human sec
19	3410.5	59.6	3770	5 AAF57551	Aaf57551 Human cal
20	3400.5	59.4	3213	4 AAS01409	Aas01409 Human sec
21	3400.5	59.4	3213	5 AAF57546	Aaf57546 Human cal
22	3326.5	58.1	3114	4 AAS01408	Aas01408 Human sec
23	3326.5	58.1	3114	5 AAF57545	Aaf57545 Human cal
24	3278.5	57.3	3057	4 AAS01407	Aas01407 Human sec
25	3278.5	57.3	3057	5 AAF57544	Aaf57544 Human cal
26	3222	56.3	3598	3 AAA09261	Aaa09261 Human alp
27	3195.5	55.8	3382	8 ABZ23112	Abz23112 Nucleotid
28	2306	40.3	1523	10 ADK41000	Adk41000 Novel hum
29	2306	40.3	1523	13 ADR15714	Adr15714 Kinase 41
30	2218	38.7	1452	3 AAA09279	Aaa09279 Human alp
31	2026.5	35.4	2008	3 AAA09260	Aaa09260 Human alp
32	1959.5	34.2	1774	3 AAZ51626	Aaz51626 Human mem
33	1792.5	31.3	1050	4 AAS01412	Aas01412 Human sec
34	1792.5	31.3	1050	5 AAF57549	Aaf57549 Human cal
35	1695	29.6	969	4 AAS01411	Aas01411 Human sec
36	1695	29.6	969	5 AAF57548	Aaf57548 Human cal
37	1598	27.9	912	4 AAS01410	Aas01410 Human sec
38	1598	27.9	912	5 AAF57547	Aaf57547 Human cal
39	1565	27.3	4892	12 AD016904	Ado16904 Tobacco b
40	1554.5	27.1	5028	12 AD016902	Ado16902 Tobacco b
41	1497.5	26.2	5862	5 AAD05208	Aad05208 D. melano
42	1410	24.6	6519	4 ABL22283	AbL22283 Drosophil
43	1392.5	24.3	4383	12 AD016900	Ado16900 Tobacco b
44	1362.5	23.8	856	4 AAS31088	Aas31088 Human dia
45	1336.5	23.3	3414	4 ABL10835	AbL10835 Drosophil

ALIGNMENTS

RESULT 1

ADF71819

ID ADF71819 standard; cDNA; 3486 BP.

XX ADF71819;

XX ADF71819;

DT 12-FEB-2004 (first entry)

XX Human calcium channel alpha2delta4 subunit cDNA.

DE Human calcium channel alpha2delta4 subunit cDNA.

XX neuroprotective; cytosolic; gene therapy; calcium channel;

KW alpha2delta-4; amyotrophic lateral sclerosis; multiple sclerosis; cancer;

XX human; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 190..3462

FT /*tag= a

FT /product= "Human calcium channel alpha2delta4 subunit"

PN US2003170785-A1.

XX 11-SEP-2003.

XX 10-APR-2002; 2002US-00119624.

XX 11-APR-2001; 2001US-00833222.

XX

PA (QINN//) QIN N.
PA (CODD//) CODD E.
PI Qin N, Codd E;
XX
DR WPI; 2003-898262/82.
DR P-PSDB; ADF71820.
XX
XX New human alpha2 delta4 calcium channel subunit protein and nucleic acid
PT molecule, useful for diagnosing and treating diseases associated with
PT defective calcium channel subunit, e.g. cancer and multiple sclerosis.
XX
PS Claim 10; SEQ ID NO 9; 37pp; English.
XX
XX The invention describes a new isolated and purified nucleic acid molecule
CC comprising: a sequence having at least a 70% identity to nucleotides 1-
CC 224 or 3308-3486 of a sequence of 3486 bp (S1) fully defined in the
CC specification; at least 15 sequential bases of the polynucleotide of (a);
CC or a sequence that is complementary to the polynucleotide of (a) or (b).
CC Specifically claimed is an alpha2delta-4 nucleic acid molecule comprising
CC a sequence of 3486 bp fully defined in the specification and encoding an
CC alpha2delta-4 calcium channel subunit protein having a sequence of 1090
CC amino acids fully defined in the specification. The nucleic acid molecule
CC and polypeptide are useful in diagnosing and treating a disease or
CC disorder associated with a defective alpha2delta-4 subunit, such as
CC ankyrotrophic lateral sclerosis, multiple sclerosis or cancer. The methods
CC may be used for identifying compounds capable of treating the above-
CC mentioned diseases or disorders. This sequence encodes human calcium
CC channel alpha2delta-4 subunit.
XX
SQ Sequence 3486 BP; 827 A; 957 C; 1009 G; 693 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 3486
Score: 5726.00 Matches: 1090
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-833-222A-10 (1-1090) x ADF71819 (1-3486)

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Db 250 GGCGGGGACCTGTATTAACACTGTGACCAATACTCAGGCTCTCTTTGCTGCAGAGAAG 309
QY 41 TyrLysAspValGluSerSerLeuLysLysLysLysLysLysLysLysLysLysLys 60
Db 310 TACAAGATGTGGAGTCCAGCTCTGAAGATCGAGAGGTGGATGGCTTTGGAGCTGGTGAGG 369
QY 61 LysPheSerGluAspMetGluAsnMetLeuArgArgLysValGluAlaValGlnAsnLeu 80
Db 370 AAGTCTCAGAGGACATGGAGAACATGCTGCGGAGGAGAAATCGAGCGGCTCCAGATCTG 429
QY 81 ValGluAlaGluGlnAlaAspLeuAsnHisGluPheAsnGluSerLeuValPheAsp 100
Db 430 GTGGAAGCTGCCGAGGAGGCGGACCTGAAACACAGAAATTCGAATCCCTGGTGTTCGAC 489
QY 101 TyrTyrAsnSerValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 120
Db 490 TATTACACTCGGTCTCTGATCAACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 549
QY 121 AlaGluPheLeuLeuGluSerAsnAlaHisPheSerAsnLeuProValAsnThrSerIle 140
Db 550 GCCGAGTTCCTCTCGGAGTCCAATGCTCACTTCAGCAACCTGCGGCTGAACACCTCCATC 609
QY 141 SerSerValGlnLeuProThrAsnValTyrAsnLysAspProAspIleLeuAsnGlyVal 160
Db 610 AGCAGCGTGCAGCTGCCCAACGTTGATCAACAAAGAGCCAGATATTTTAAATGGAGTC 669

QY 161 TyrMetSerGluAlaLeuAsnAlaValPheValGluAsnPheGlnArgAspProThrLeu 180
Db 670 TACATGTCTGAAGCCTTGAATGCTGTCTTCGTGGAGAACTTCAGAGAGACCCCAACGTTG 729
QY 181 ThrTrpGlnTyrPheGlySerAlaThrGlyPhePheArgIleTyrProGlyIleLysTrp 200
Db 730 ACCTGGCAATATTTGGCAGTGCNACTGGATCTTTCAGGATCTATCCAGGTATAAATGG 789
QY 201 ThrProAspGluAsnGlyValIleThrPheAspCysArgAsnArgGlyTrpTyrIleGln 220
Db 790 ACACCTGTATGAGAATGGAGTCACTTTTACTGCGGAAACCGCGCTGTGATCAATCAA 849
QY 221 AlaAlaThrSerProLysAspIleValIleLeuValAspValSerGlySerMetLysGly 240
Db 850 GCTGCTACTTCTCCCAAGGACATAGTGATTTTGGTGACGTGAGCGGAGATATGAAGGG 909
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Db 910 CTGAGGATGACTATTTCGCAAGCACACCATCACCACCATCTTGGACACCTTGGGGGAGAT 969
QY 261 AspPheValAsnIleIleAlaTyrAsnAspTyrValHisTyrIleGluProCysPheLys 280
Db 970 GACTTCGTTTAATATCATAGCTACATGACTACGCTCATTTACATCGAGCCTTGTGTTAAA 1029
QY 281 GlyIleLeuValGlnAlaAspArgAsnArgGluHisPheLysLeuLeuValGluGlu 300
Db 1030 GGATCTCTCGTCAGCGGAGCAGACATCGAGACATTTCAACTGCTGTGTGGAGGAG 1089
QY 301 LeuMetValLysGlyValGlyValValAspGlnAlaLeuArgGluAlaPheGlnIleLeu 320
Db 1090 TTGATGGTCAAGAGTGTGGGGTGTGGACCAAGCCCTCAGAGAAAGCTTCCAGATCCTG 1149
QY 321 LysGlnPheGlnGluAlaLysGlnGlySerLeuCysAsnGlnAlaIleMetLeuIleSer 340
Db 1150 AAGCAGATTTCCAAAGGCGCAAGCAAGAGCCCTCTGCAACGAGGCCATCATGCTCATCAGC 1209
QY 341 AspGlyAlaValGluAspTyrGluProValPheGluLysTyrAsnTrpProAspCysLys 360
Db 1210 GACGGCGCGTGGAGGACTACGAGCGCGTGTGTGAGAAGTATTAACCTGGCCAGACTGTAAG 1269
QY 361 ValArgValPheThrTyrLeuIleGlyArgGluValSerPheAlaAspArgMetLysTrp 380
Db 1270 GTCCGAGTTTTTCACTTACCTATTGGGAGAGAAGTGTCTTTTGTCTACCGCATGAAGTGG 1329
QY 381 IleAlaCysAsnLysGlyTyrTyrThrGlnIleSerThrIleAlaAspThrGlnGlu 400
Db 1330 ATTGCATGCAACAACAAAGGCTACTACACGCAAGTCTCAACGCTGGCGGACACCCAGGAG 1389
QY 401 AsnValMetGluTyrLeuHisValLeuSerArgProMetValIleAsnHisAspHisAsp 420
Db 1390 AACGTGATGGAAATCTCTGCACGTGTCTACCGCGCCCATGGTCTNCAACCAACGACACGAC 1449
QY 421 IleIleTrpThrGluAlaTyrMetAspSerLysLeuLeuSerSerGlnAlaGlnSerLeu 440
Db 1450 ATCATCTGGACAGAGGCTTACATGGACAGCAAGCTCCTCAGCTCGCAGGCTCAGAGCCTG 1509
QY 441 ThrLeuLeuThrThrValAlaMetProValPheSerLysLysAsnGluThrArgSerHis 460
Db 1510 ACACCTGCTCACCACCTGTGGCCATGGCAGTCTTCAGCAAGAAGAACGAAACGCGATCCCAT 1569
QY 461 GlyIleLeuLeuGlyValValGlySerAspValAlaLeuArgGluLeuMetLysLeuAla 480
Db 1570 GGCATTTCTCTGGGTGTGGTGGCTCAGATGTGGCCCTCAGAGAGCTGATGAAGCTGGCG 1629
QY 481 ProArgTyrLysLeuGlyValHisGlyTyrAlaPheLeuAsnThrAsnAsnGlyTyrIle 500
Db 1630 CCCCAGTCAAGCTTGGAGTGCACGATACGCTTCTTCTGAACACCAACCAATGGCTACATC 1689
QY 501 LeuSerHisProAspLeuArgProLeuTyrArgGluGlyLysLysLysLysLysLysLys 520
Db 1690 CTCTCCCATCCCGACTCCGGCCCCCTGTGTACAGAGAGGGGAGAAACTTAAACCCCAACCT 1749

Qy 521 AsnTyrAsnSerValAspLeuSerGluValGluTrpGluAspGlnAlaGluSerLeuArg 540
 Db 1750 AACTACAAACAGTGTGGATCTCTCCGAAGTGGAGTGGGAAGACCAAGCGGTGAATCTCTCAGA 1809
 Qy 541 ThrAlaMetIleAsnArgGluThrGlyThrLeuSerMetAspValLysValProMetAsp 560
 Db 1810 ACAGCCATGATCAATAGGGAACAGGTACTCTCTCGATGGATGTGAAGGTTCAGATGGAT 1869
 Qy 561 LysGlyLysArgValLeuPheLeuThrAsnAspTyrPhePheThrAspIleSerAspThr 580
 Db 1870 AAGGGAAGCGAGTCTCTTCTGACCAATGACTACTTCTTACGGACATCAGCGACACC 1929
 Qy 581 ProPheSerLeuGlyAlaValLeuSerArgGlyHisGlyGluTyrIleLeuLeuGlyAsn 600
 Db 1930 CCTTTCAGTTGGGGGGGGTCTCTCCGGGGCCACGGAGAATACATCTCTTCTGGGGAAC 1989
 Qy 601 ThrSerValGluGluGlyLeuHisAspLeuLeuHisProAspLeuAlaLeuAlaGlyAsp 620
 Db 1990 ACGTCTGTGGNAGAGCGCTGCACTTGTCTTCCACGAGACCTGGCCCTGGCCGGTGAC 2049
 Qy 621 TrpIleTyrCysIleThrAspIleAspProAspHisArgLysLysLeuSerGlnLeuGluAla 640
 Db 2050 TGGATCTACTGCATCAGATATATTGACCCAGACCACCGGAAGCTCAGCCAGCTAGAGGCC 2109
 Qy 641 MetIleArgPheLeuThrArgLysAspProAspLeuGluCysAspGluGluLeuValArg 660
 Db 2110 ATGATCCGCTTCTTCACGAGAGGAGCCAGACCTGGAGTGTGACGAGGAGCTGGTCCGG 2169
 Qy 661 GluValLeuPheAspAlaValThrAlaProMetGluAlaTyrTrpThrAlaLeuAla 680
 Db 2170 GAGTGTCTGTTGACGGGTGGTGACAGCCCCCATGGNAGCCTACTGGACAGCGCTGGCC 2229
 Qy 681 LeuAsnMetSerGluGluSerGluHisValValAspMetAlaPheLeuGlyThrArgAla 700
 Db 2230 CTCAACATGTCGAGGAGTCTGAACACGCTGGTGACATGGCTTCTCTGGGCACCCGGCT 2289
 Qy 701 GlyLeuLeuArgSerLeuPheValGlySerGluLysValSerAspArgLysPheLeu 720
 Db 2290 GGCTCTCTGAGAGCAGCTGTTCTCGTGGGTCTCCGAGAAGGTCTCCGACAGGAAGTTCCTG 2349
 Qy 721 ThrProGluAspGluAlaSerValPheThrLeuAspArgPheProLeuTyrTrpArgGln 740
 Db 2350 ACACCTGAGGACGAGGCGAGGTGTTCAACCCTGACCGCTTCCCGCTGTGGTACCGCCAG 2409
 Qy 741 AlaSerGluHisProAlaGlySerPheValPheAsnLeuArgTrpAlaGluGlyProGlu 760
 Db 2410 GCCTCAGAGCATCTGCTGGCAGCTCTGCTTCAACCTCCGCTGGCGAGAAGACAGAA 2469
 Qy 761 SerAlaGlyGluProMetValValThrAlaSerThrAlaValAlaValThrValAspLys 780
 Db 2470 AGTGGGGTGAACCCATGGTGTGACGGCAAGCACAGCTGTGGCGGTGACCGTGGAAGA 2529
 Qy 781 ArgThrAlaIleAlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLys 800
 Db 2530 AGGACACCATTTGCTGAGCGCGGGGTCCAAATGAAGTGGAAATTCCTCCAGCGCAAA 2589
 Qy 801 PheTrpAlaAlaThrArgGlnCysSerThrValAspGlyProTyrThrGlnSerCysGlu 820
 Db 2590 TTCTGGCGGCAACCGCGCAGTGCAGCACGTGTGATGGCGGTATACACAGAGCTGGAG 2649
 Qy 821 AspSerAspLeuAspCysPheValIleAspAsnAsnGlyPheIleLeuIleSerLysArg 840
 Db 2650 GACAGTGATCTGGACTGCTTCTGTCATCGACACAAACCGGTTCAATCTTGATCTCCAGAGG 2709
 Qy 841 SerArgGluThrGlyArgPheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeu 860
 Db 2710 TCCGAGAGAGCGGAAGATTCTGGGGAGGTGGTGTGCTGTCTGTGACCCAGCTGCTC 2769
 Qy 861 SerMetGlyValPheSerGlnValThrMetTyrAspTyrGlnAlaMetCysLysProSer 880
 Db 2770 AGCATGGGGTGTTCAGCGAAGTGAATGTATGATGACTATCAGGCGCATGTGCAAAACCTCG 2829
 Qy 881 SerHisHisSerAlaAlaGlnProLeuValSerProIleSerAlaPheLeuThrAla 900

Db 2830 AGTCACCACACAGTCAGCCCGAGCCCTGGTCAGCCCAATTTCTGCTTCTTGTACCGCG 2889
 Qy 901 ThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLeuGluTrpSerValTrpGlySer 920
 Db 2890 ACCAGTGGTGTCTGACGAGCTGGTGTCTTCTGCTGGAGTGGAGTGTCTGGGGCTCC 2949
 Qy 921 TrpTyrAspArgGlyAlaGluAlaLysSerValPheHisHisSerHisLysLysLys 940
 Db 2950 TGGTACGACAGAGGGCCGAGGCCAAAGTGTCTTCCATCACTCCCAACCAACAAG 3009
 Qy 941 GlnAspProLeuGlnProCysAspThrGluTyrProValPheValTyrGlnProAlaIle 960
 Db 3010 CAGACCCGCTGACGCCCTCGACACGAGTACCCCGTGTGTGTACACCGCCCATC 3069
 Qy 961 ArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLysValPheValValGlnGln 980
 Db 3070 CGGGAGGCCAACGGATCGTGGAGTGGGGCCCTGCCAGAAAGTATTTGTGGTCAGCAG 3129
 Qy 981 IleProAsnSerAsnLeuLeuLeuValThrAspProThrCysAspCysSerIlePhe 1000
 Db 3130 ATTCCCAACAGTAACCTCTCTCTCTGGTGACAGACCCACCTGTGACTGCAGCATCTTC 3189
 Qy 1001 ProProValLeuGlnGluAlaThrGluValLysTyrAsnAlaSerValLysCysAspArg 1020
 Db 3190 CCACCACTGTGACGAGGCGACAGAGTCAAAATATATGCTCTGTCAAAATGTGACCGG 3249
 Qy 1021 MetArgSerGlnLysLeuArgArgProAspSerCysHisAlaPheHisProGluVal 1040
 Db 3250 ATGGCTCTCCAGAAAGCTCCCGCGGACACAGACTCTCTGCCACCGCTTCCATCCAGAGGTG 3309
 Qy 1041 ArgValGluAlaAspArgGlyTrpAlaGlyPheSerSerProAsnProLeuCysLeuGly 1060
 Db 3310 CGGGTTGAGCGGATCGAGGTGGGTGGATTTTCATCCCAAAACCCCTCTGTGCTGGT 3369
 Qy 1061 LeuCysProCysArgGlnGluHisIleGlyMetProMetAsnThrProValProValLeu 1080
 Db 3370 CTGTGCCCTGACAGAGGAGCATATAGGATGCCAATGAACACACCTGTGCTGTGCTT 3429
 Qy 1081 LeuGlyGlyAsnIleArgValTyrAlaLeu 1090
 Db 3430 CTGGGGGAAACATTCGCGTTTATGCCCTG 3459

RESULT 2
 ABZ20598
 ID ABZ20598 standard; cDNA; 3486 BP.
 XX AC ABZ20598;
 XX AC ABZ20598;
 XX 03-MAR-2003 (first entry)
 XX Human voltage gated calcium channel alpha2delta-4 subunit cDNA.
 DE Human;
 KW Human; voltage gated calcium channel; alpha2delta-4 subunit;
 KW antiparkinsonian; tranquilizer; neuroprotective; anticonvulsant;
 KW antimigraine; analgesic; cyostatic; antidepressant; antiinflammatory;
 KW gene therapy; epilepsy; migraine; ataxia; vestibular defect;
 KW chronic pain; neuropathic pain; Parkinson's disease; depression; cancer;
 KW inflammation; seizure-related syndrome; anxiety; multiple sclerosis; ss.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 PH CDS 190..3462
 FT /*tag= a
 FT /product= "calcium channel alpha2delta-4 subunit"
 XX
 PN WO200283947-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US011297.
 XX

PR 11-APR-2001; 2001US-00833222.
XX (ORTH) ORTHO-MCNEIL PHARM INC.
XX Qin N, Codd E;
XX WPI; 2003-093006/08.
DR P-PSDB; ABP59509.
XX
PT New nucleic acid molecule encoding human alpha2 delta4 calcium channel
PT subunit protein, useful for diagnosing and treating a disease associated
PT with defects in the subunit protein, e.g. epilepsy, migraine, ataxia or
PT chronic pain.
XX
PS Claim 1; Page 56-59; 91pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC voltage gated calcium channel alpha2delta-4 subunit. The sequences are
CC useful for diagnosing and treating a disease or disorder associated with
CC a defective alpha2delta-4 subunit, such as seizure-related syndromes,
CC epilepsy, migraine, ataxia, vestibular defects, chronic pain, neuropathic
CC pain, mood, sleep interference, anxiety, AIDS, multiple sclerosis, mania,
CC Parkinson's disease, substance abuse/addiction syndromes, depression,
CC cancer, or inflammation. The present sequence is the coding sequence of
CC the invention
XX
SQ Sequence 3486 BP; 827 A; 957 C; 1009 G; 693 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 3486
Score: 5726.00 Matches: 1090
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-833-222a-10 (1-1090) x ABZ20598 (1-3486)

Qy 1 MetAlaValAlaLeuGlyThrArgAtgAspArgValLysLeuTrpAlaAspThrPhe 20
Db 190 ATGGCTGTAGCTTTAGGGA CAAGAGAGGAGGAGAGTGAAGCTATGGGCTGACACCTTC 249

Qy 21 GlyGlyAspLeuThrValThrLysTyrSerGlySerLeuLeuLeuGlnLysLys 40
Db 250 GGCGGGACCTGTATAACACTGTGACCAATATACTCAGGCTCTCTCTTGTCTGCAGAGAGAG 309

Qy 41 TyrLysAspValGluSerSerLeuLysIleGluGluValAspGlyLeuGluLeuValArg 60
Db 310 TACAAGGATGTGGAGTCCAGTCTGAAGATCGAGGAGGTGGATGGCTTGGAGCTGGTGAGG 369

Qy 61 LysPheSerGluAspMetGluAsnMetLeuArgArgLysValGluAlaValGlnAsnLeu 80
Db 370 AAGTTCTCAGAGACATGGAGAACATGCTCGGAGGAGAAAGTCAGGCGGTCCAGAAATCTG 429

Qy 81 ValGluAlaAlaGluGluAlaAspLeuAsnHisGluPheAsnGluSerLeuValPheAsp 100
Db 430 GTGGAAGCTGCCGAGGAGGCGGACCTGAACCAAGATTCATGAATCCCTGGTGTTCGAC 489

Qy 101 TyrTyrAsnSerValLeuIleAsnGluArgAspGluLysGlyAsnPheValGluLeuGly 120
Db 490 TATTACAACTCCGTCCTGTATCAACAGAGAGGAGGAGCAAGGCAACTTCGTGGAGCTGGGC 549

Qy 121 AlaGluPheLeuLeuGluSerAsnAlaHisPheSerAsnLeuProValAsnThrSerIle 140
Db 550 GCCGAGTTCTCTGGAGTCCAATGCTTCACTTCAGCAACTCGCGGTGAACACCTCCATC 609

Qy 141 SerSerValGlnLeuProThrAsnValTyrAsnLysAspProAspIleLeuAsnGlyVal 160
Db 610 AGCAGCGTGCAGCTGCCCAACGCTGTACAACAAAGAGCCAGATATTTAAATGGAGTC 669

Qy 161 TyrMetSerGluAlaLeuAsnAlaValPheValGluAsnPheGlnArgAspProThrLeu 180
Db 670 TACATGTCGAAGCCTTGAATGCTGCTTCTCGTGAGAACTTCCAGAGAGACCCCAACGTTG 729

Qy 181 ThrTrpGlnTyrPheGlySerAlaThrGlyPheArgIleTyrProGlyIleLysTrp 200
Db 730 ACCTGGCAATATTTGGCAGTGCACACTGGATTCTTCAGGATCTATCCAGGTATATAAATGG 789

Qy 201 ThrProAspGluAsnGlyValIleThrPheAspCysArgAsnArgGlyTyrTrpIleGln 220
Db 790 ACACCTGATGAGAAATGGAGTCATTCTTTGACTGCCGAAACCGCGCTGTATCATTTCAA 849

Qy 221 AlaAlaThrSerProLysAspIleValIleLeuValAspValSerGlySerMetLysGly 240
Db 850 GCTGCTACTTCTCCCAAGGACATAGTCAATTTGGTGACGTCGAGCGCAGTATGAAGGGG 909

Qy 241 LeuArgMetThrIleAlaLysHisThrIleThrIleLeuAspThrLeuGlyGluAsn 260
Db 910 CTGAGATGACTATATGCCAAGCACACCATCACCACCATCTTGACACCCCTGGGGGAGAAAT 969

Qy 261 AspPheValAsnIleAlaTyrAsnAspTyrValHisTyrIleGluProCysPheLys 280
Db 970 GACTTCGTTAATATCATAGCGTACATGACTACGTCCATTACATCGAGCCTTGTTTTAA 1029

Qy 281 GlyIleLeuValGlnAlaAspArgAsnArgGluHisPheLysLeuLeuValGluGlu 300
Db 1030 GGGATCTCTGTCAGGCGGACCGAGACAATCGAGAGCATTTCAAACTGCTGCTGGAGGAG 1089

Qy 301 LeuMetValLysGlyValGlyValValAspGlnAlaLeuArgGluAlaPheGlnIleLeu 320
Db 1090 TTGATGTCAAAGGTGTGGGTCTGGACCAAGCCCTTGAGAGAGCCTTCAGATCCTG 1149

Qy 321 LysGlnPheGlnGluAlaLysGlnGlySerLeuCysAsnGlnAlaIleMetLeuIleSer 340
Db 1150 AAGCAGTTCCAAAGAGGCCAAGCAAGAGCCTCTGCAACCCAGGCCATCATGCTCATCAGC 1209

Qy 341 AspGlyAlaValGluAspTyrGluProValPheGluLysTyrAsnTrpProAspCysLys 360
Db 1210 GACGCGCGCTGGAGGACTACGAGCGGTGTTTGAAGATATAACTGGCCAGACTGTGAAG 1269

Qy 361 ValArgValPheThrTrpLeuIleGlyArgGluValSerPheAlaAspArgMetLysTrp 380
Db 1270 GTCCGAGTTTTCACCTTACCTCATTTGGGAGAGAGTGTCTTTTGTCTACCGCATGAAGTGG 1329

Qy 381 IleAlaCysAsnAsnLysGlyTyrTyrThrGlnIleSerThrLeuAlaAspThrGlnGlu 400
Db 1330 ATTGTCATCAACAACAAGGCTACTACACGAGATCTCAACGCTGGCGGACACCCAGGAG 1389

Qy 401 AsnValMetGluTyrLeuHisValLeuSerArgProMetValIleAsnHisAspHisAsp 420
Db 1390 AACGTCATGGAATACCTGCACGCTGCTCAGCCGCCCATGGTTCATCAACCAACGACCGAC 1449

Qy 421 IleIleTrpThrGluAlaTyrMetAspSerLysLeuLeuSerSerGlnAlaGlnSerLeu 440
Db 1450 ATCACTGCAGAGAGGCTTACATGGACACAGCTCTCTCAGCTCGGCGCTCAGAGCCTG 1509

Qy 441 ThrLeuLeuThrThrValAlaMetProValPheSerLysLysAsnGluThrArgSerHis 460
Db 1510 ACACTGCTCACCATGTGTGCCATGTCAGTCTTCAGCAAGAAGAACCAACCGCATCCCAT 1569

Qy 461 GlyIleLeuLeuGlyValValGlySerAspValAlaLeuArgGluLeuMetLysLeuAla 480
Db 1570 GGCATTCTCTCGGTGTGGTGGGCTCAGATGTGGCCCTGAGAGAGCTGATGAAGCTGGCG 1629

Qy 481 ProArgTyrLysLeuGlyValHisGlyTyrAlaPheLeuAsnThrAsnAsnGlyTyrIle 500
Db 1630 CCCCCTGACAACTGGAGTGCAGGATACGCTTCTGCACACCAACCAATGGCTACATC 1689

Qy 501 LeuSerHisProAspLeuArgProLeuTyrArgGluGlyLysLysLysProLysPro 520
Db 1690 CTCTCCATCCGACCTCCGCGCCCTGTACAGAGAGGGAAGAACTAAACCCCAACCT 1749

Qy 521 AsnTyrAsnSerValAspLeuSerGluValGluTrpGluAspGlnAlaGluSerLeuArg 540
Db 1750 AACTACACAGTGTGGATCTCTCCGAAGTGGAGTGGGAAGACGAGCTGAATCTCTGAGA 1809

541 ThrAlaMetIleAenArgGluThrGlyThrLeuSerMetAspVallylsValProMetAsp 560
1810 ACAGCCATGATCAATAGGAAACAGGTACTCTCTCGATGGATGTGAAGGTTCCGATGGAT 1869
561 LysGlyValArgValLeuPheLeuThrAsnAspTyrPhePheThrAspIleSerAspThr 580
1870 AAAGGAAGCGAGGTCTTCTCCTGACCAATGACTACTTCTTCACGGACATCAGGCACCC 1929
581 ProPheSerLeuGlyAlaValLeuSerArgGlyHisGlyGluTyrIleLeuLeuGlyAsn 600
1930 CCTTTCAGTTTGGGGCGGTGCTGCTCCGGCGCCACCGAGAAATACATCCTTCTGGGGAAC 1989
601 ThrSerValGluGluGlyLeuHisAspLeuLeuHisProAspLeuAlaLeuAlaGlyAsp 620
1990 ACGTCTGTGAAGAAGCCCTGCTGCTGCTTCCACCCAGACCTGGCCCTGGCCGCTGAC 2049
621 TrpIleTyrCysIleThrAspIleAspProAspHisArgIleValLeuSerGlnLeuGluAla 640
2050 TGGATCTACTGTCATCAGATATTGACCCAGACCACCGAAGCTCAGCCAGCTAGAGGCC 2109
641 MetIleArgPheLeuThrArgLysAspProAspLeuGluCysAspGluGluLeuValArg 660
2110 ATGATCCGCTTCTCACCAGGAAGGACCCAGACCTGGAGTGTGACGAGGAGCTGGTCCGG 2169
661 GluValLeuPheAspAlaValValThrAlaProMetGluAlaTyrTrpThrAlaLeuAla 680
2170 GAGGTGCTGTTTGAACGGCGGTGTGACAGCCGCCATGGAAGCCTACTGACAGAGCCTGGCC 2229
681 LeuAsnMetSerGluGluSerGluHisValValAspMetAlaPheLeuGlyThrArgAla 700
2230 CTCAACATGTCCGAGGAGTCTGAACACGTTGTGTGACATGGCTTCTCTGGGACCCCGGGCT 2289
701 GlyLeuLeuArgSerSerLeuPheValGlySerGluLysValSerAspArgLysPheLeu 720
2290 GGCTCTCTGAGACGACGCTGTTCTGCGGCTCCGAGAGTCTCCGACAGAGATTCCTG 2349
721 ThrProGluAspGluAlaSerValPheThrLeuAspArgPheProLeuTyrTrpArgGln 740
2350 ACACCTGAGGACGAGGCGAGCGTGTTCACCCCTGGACCGCTTCCCGCTGTGTATCCGCGCAG 2409
741 AlaSerGluHisProAlaGlySerPheValPheAsnLeuArgTrpAlaGluGlyProGlu 760
2410 GCCTCAGAGCATCTGCTGGCAGCTTCTGTTCAACCTCCGCTGGGCGAGAGGACCAAGAA 2469
761 SerAlaGlyGluProMetValValThrAlaSerThrAlaValAlaValThrValAspLys 780
2470 AGTGGGGTGNACCCATGGTGGTGACCGCAAGCACACCTGTGGCGGTGACCGTGGACAAG 2529
781 ArgThrAlaIleAlaAlaAlaAlaGlyValGlnMetLysLeuGluPheLeuGlnArgLys 800
2530 AGGACAGCCATTGCTGCAGCGCGCGGCGTCCAAATGAAGCTGGAATTCCTCCAGCGCAAA 2589
801 PheTrpAlaThrArgGlnCysSerThrValAspGlyProTyrThrGlnSerCysGlu 820
2590 TTCTGGGCGGCAACCGCGCAGTGCAGCAGCTGTGATGGGCGGTACACACAGAGCTGGCAG 2649
821 AspSerAspLeuAspCysPheValIleAspAsnAsnGlyPheIleLeuIleSerLysArg 840
2650 GACAGTATCTGACTGCTTCGTCATCGACACACAAACCGGTTCAATCTGATCTCCAAGAGG 2709
841 SerArgGluThrGlyArgPheLeuGlyGluValAspGlyAlaValLeuThrGlnLeuLeu 860
2710 TCCCGAGAGACGGGAAGATTTCTGGGGAGGTGGATGCTGTCTCTGACCCAGCTGCTC 2769
861 SerMetGlyValPheSerGlnValThrMetTyrAspTyrGlnAlaMetCysLysProSer 880
2770 AGCATGGGGGTTCACCCCAAGTACTATGTATGACTATCAGGCCATGTGCAAAACCCCTCG 2829
881 SerHisHisSerAlaAlaGlnProLeuValSerProIleSerAlaPheLeuThrAla 900
2830 AGTCACCACACAGTCAGGCCACCCCTGCTGACGCCAATTTCTGCTCTTCTTGACGGCG 2889
901 ThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLeuGluTrpSerValTrpGlySer 920

2890 ACCAGTGGCTGCTGCAGGAGCTGGTGTCTCTGCTGAGTGGAGTGTCTGGGGCTCC 2949
921 TrpTyrAspArgGlyAlaGluAlaLysSerValPheHisHisSerHisLysHisLysLys 940
2950 TGGTACGACAGAGGGCGGAGGCCAAAGTGTCTTCATCTCACTCCCAACAACAACAAG 3009
941 GlnAspProLeuGlnProCysAspThrGluTyrProValPheValTyrGlnProAlaIle 960
3010 CAGGACCCGCTGCAGGCCCTCGCACAGGAGTACCCCGTGTCTGTTGACGAGCCGCCATC 3069
961 ArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLysValPheValGlnGln 980
3070 CGGAGGCCAACGGGATCGTGGAGTGGGGCCCTGCCAGAAAGTATTTGGTGCAGCAG 3129
981 IleProAsnSerAsnLeuLeuLeuValThrAspProThrCysAspCysSerIlePhe 1000
3130 ATTCCCAACAGTAACCTCTCTCTGCTGACAGACCCCACTGTGACTGCAGCATCTTC 3189
1001 ProProValLeuGlnGluAlaThrGluValLysTyrAsnAlaSerValLysCysAspArg 1020
3190 CCACCACTGCTGCAGGAGGCGACAGAAATCAATATAATGCCTCTGTCAAATGTGACCGG 3249
1021 MetArgSerGlnLysLeuArgArgProAspSerCysHisAlaPheHisProGluVal 1040
3250 ATGCGCTCCAGAAAGTCCGCGGCGACCAAGCTCTCTGCCACGCTTCCATCCAGAGGTG 3309
1041 ArgValGluAlaAspArgGlyTrpAlaGlyPheSerSerProAsnProLeuCysLeuGly 1060
3310 CGGGTTGAGGCGGATCGAGGCTGGGTGGATTTTCATCCCAAAACCTCTGTGCTGGGT 3369
1061 LeuCysProCysArgGlnGluHisIleGlyMetProMetAsnThrProValProValLeu 1080
3370 CTGTGCCCCCTGCAGACAGGAGCATATAGGATGCCAATGAACACACACCTGTGCTGTCTT 3429
1081 LeuGlyGlyAsnIleArgValTyrAlaLeu 1090
3430 CTCGGGGGAAACATTCGCGTTTATGCCCTG 3459
RESULT 3
AAA09254
ID AAA09254 standard; cDNA; 5073 BP.
XX AAA09254;
XX DT 10-AUG-2000 (first entry)
XX Human alpha-2-delta-D gene.
XX alpha-2-delta-D; calcium channel; 12p13.3; gabapentin; cytostatic;
KW anticonvulsant; antimigrane; antiparkinsonian; antidepressant; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
FT CDS 3..3365
FT FT /*tag= a
PN WO200020450-A2.
XX 13-APR-2000.
XX PF 07-OCT-1999; 99WO-US023519.
XX PR 07-OCT-1998; 98US-0103322P.
XX PR 30-OCT-1998; 98US-0106473P.
XX PR 28-DEC-1998; 98US-0114088P.
XX (WARN) WARNER LAMBERT CO.
XX PA Johns MA, Moldover B, Offord JD;
XX PI WPI; 2000-303744/26.
XX DR

Claim 1; SEQ ID NO 176; 1177pp; English.

The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present DNA sequence represents a gene of the invention.

Sequence 4841 BP; 1176 A; 1335 C; 1339 G; 991 T; 0 U; 0 Other;

Alignment Scores:

Pred. NO.:	0	Length:	4841
Score:	5385.50	Matches:	1034
Percent Similarity:	97.47%	Conservative:	5
Best Local Similarity:	97.00%	Mismatches:	27
Query Match:	94.05%	Indels:	1
DB:	10	Gaps:	0

US-09-833-222A-10 (1-1090) x ADE07110 (1-4841)

Qy	11	AspArgValIysLeuTrpAlaAspThrPheGlyAspLeuTyrAsnThrValThrLys	30
Db	498	GAACAGTGAAGCTATGGCTGCACACCTTCGGCGGGACCTGTATAACACTGTGACCAA	557
Qy	31	TyrSerGlySerLeuLeuLeuGlnIlysIystrIyAspValGluSerSerLeuIlyle	50
Db	558	TACTTCAGGCTCTCTTCCTGCTGCAGAGAAGTACAAAGATGTGGAGTCCAGTCTGAAGATC	617
Qy	51	GluGluValAspGlyLeuGluLeuValArgIyAspPheSerGluAspMetGluAsnMetLeu	70
Db	618	GAGAGGTGGATGCTTGGAGCTGGTGGAGAGTTCTCAGAGGACATGGAGAACATGCTG	677
Qy	71	ArgArgIySValGluAlaValAlnAsnLeuValGluAlaGluGluAlaAspLeuAsn	90
Db	678	CGGAGGAAAGTCGAGGCGGTCCAGAACTCGTGTGAAGCTGCCGAGGAGGCCGACCTGAAC	737
Qy	91	HisGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArg	110
Db	738	CACGAATTCAATGAATCCCTGGTGTTCGACTATTACAACTCGGTCTGTATCAACGAGAGG	797
Qy	111	AspGluIySgIyAsnPheValGluLeuGlyAlaGluPheIleuLeuGluSerAsnAlaHis	130
Db	798	GACGAGAAGGGCAACTTCGTGGAGCTGGGCGCCAGTTCCTCTCGAGTCCCAATGCTCTAC	857
Qy	131	PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr	150
Db	858	TTTACGAACCTGCCGGTGAACACCTCCATCAGACGCTGCAGCTGCCACCAACGCTGAC	917
Qy	151	AsnIySAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe	170
Db	918	AACAAAGACCCAGATATTTAAATGGAGTCTACATGCTGAGCGCTTGAATGCTGCTTC	977
Qy	171	ValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGly	190
Db	978	GTGGAGAACTTCAGAGAGACCCCAACGTTGACCTGGCAATATTTTGGCAGTGCACCTGGA	1037
Qy	191	PhePheArgIleTyrProGlyIleIySTrpThrProAspGluAsnGlyValIleThrPhe	210
Db	1038	TTCTTTCAGGATCTATCCAGGTATAAATGGACACCTGATGAGATGGAGTCATTACTCTTT	1097
Qy	211	AspCysArgAsnArgGlyTrpTyrIleGlnAlaAlaThrSerProIySAspIleValIle	230
Db	1098	GACTGCCGAACCCGGCTGGTATTCACAGCTGCTACTTCTCCCAAGGACATAGTGATT	1157
Qy	231	LeuValAspValSerGlySerMetIySgIyLeuArgMetThrIleAlaIySHisThrIle	250
Db	1158	TTGGTGACGTGACGGCAGTATGAAGGGCTGAGGATGACTATTGCGAAGCACACCATC	1217
Qy	251	ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp	270


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Qy 631 AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro 650
Db 2358 GACCACCGAAGCTCAGCAGCTAGAGCCATGATCCGCTTCCTCACAGGAGGCCCA 2417
Qy 651 AspleuGluCysAspGluGluValArgGluValLeuPheAspAlaValValThrAla 670
Db 2418 GACCTGAGGTGTGACGAGGAGCTGGTCCGGAGAGTGTGTTGACGGGGTGTGACAGCC 2477
Qy 671 ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAenMetSerGluGluSerGluHisVal 690
Db 2478 CCCATGGAGGCTACTGGACAGCGCTGGCCCTCAACATGTCCGAGGAGTCTGAACACGTG 2537
Qy 691 ValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGly 710
Db 2538 GTGGACATGGCTTCTCTGGGCACCGCGCTGGCCCTCTCTGAGAAGCAGCTTGTCTGGTGGC 2597
Qy 711 SerGluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThr 730
Db 2598 TCCGAGAGGCTCTCCGACAGGAAGTTCCTGACACCTGAGGACGAGGCCAGCTGTTCACC 2657
Qy 731 LeuAspArgPheProLeuTyrTrpArgGlnAlaSerGluHisProAlaGlySerPheVal 750
Db 2658 CTGGACCGCTTCCCGCTGTGTGTACCGCCAGGCCCTCAGAGCATCTCTGTGGCAGCTTCGTC 2717
Qy 751 PheAenLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAla 770
Db 2718 TTCAACCTCGCTGGCGAGAGGACCAAGTGGGGTGAACCCATGGTGGTGACGGCA 2777
Qy 771 SerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaGlyVal 790
Db 2778 AGCACAGCTGTGGCGGTGACCGTGGACAAGAGGACAGCCATCTGTGACGCGCGGGGCTC 2837
Qy 791 GlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThr 810
Db 2838 CAAATGAAGCTGGAAATTCCTCCAGCGCANATTCCTGGCGGCGCAACCGCGCAGTGACGACT 2897
Qy 811 ValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAsp 830
Db 2898 GTGGATGGCGCGTGACACACAGAGCTGGCGAGCAGTGTATCTGGACTGCTTCGTTCATCGAC 2957
Qy 831 AsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGlu 850
Db 2958 AACAAACGGGTTCATCTGATCTCCAAAGGTGCCGAGAGCGGGAAGATTCTCGGGGAG 3017
Qy 851 ValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMet 870
Db 3018 GTGGATGGTGTCTCTGACCCAGCTGTCAGCATGGGGTGTTCAGCCAAAGTGACTATG 3077
Qy 871 TyrAspTyrGlnAlaMetCysLysProSerSerHisHisSerAlaAlaGlnProLeu 890
Db 3078 TATGACTATCAGGCCATGTGCAAAACCTCGAGTCACCACACAGTCGAGCCCGCCCGCTG 3137
Qy 891 ValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnLeuValLeu 910
Db 3138 GTCAGCCCAATTTCTGCTCTTCAACGCGCACCAAGTGGCTGTGTCAGGAGCTGTGCTG 3197
Qy 911 PheLeuLeuGluTyrSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSer 930
Db 3198 TTCTGTCTGGAGTGGAGTGTCTGGGGCTCTCTGTGTACACAGAGGGGGCGGACCAAGT 3257
Qy 931 ValPheHisHisSerHisLysHisLysGlnAspProLeuGlnProCysAspThrGlu 950
Db 3258 GTCTTCCATCACTCCCAACAACACAGAGGAGGACCGCTGACAGCCCTGCGACACCGAG 3317
Qy 951 TyrProValPheValTyrGlnProAlaIleArgGluAlaAenGlyIleValGluCysGly 970
Db 3318 TACCCCGTGTTCGTGTACCAAGCGGCGCATCCGGAGAGCCCAACGGGATCGTGGAGTGGGG 3377
Qy 971 ProCysGlnLysValPheValValGlnGlnIleProAenSerAenLeuLeuLeuVal 990
Db 3378 CCCTGCCAAGAGGTATTTGTGGTGCAGCAGGATTCCTCCCAACAGTAACTCTCTCTCTG 3437
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Qy 991 ThrAspProThrCysAspCysSerIlePheProProValLeuGlnGluAlaThrGluVal 1010
Db 3438 ACAGACCCCACTGTGCTACTGCAGCATCTTCCACCACTGTGCAGGAGGGACAGAAGTC 3497
Qy 1011 LysTyrAenAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArgPro 1030
Db 3498 AAATATATATGCTTGTCAAAATGTACCGGATGGCTTCCAGAGCTCCCGCGGACCA 3557
Qy 1031 AspSerCysHisAlaPheHisProGluValArgValGluAlaAenArgGlyTrpAlaGly 1050
Db 3558 GACTCTCTCCACGCTTCCATCCAGAGGAGAAATGCCAGGACTGCGGCGCGCTCGAC 3617
Qy 1051 PheSerSerProAenProLeuCysLeuGlyLeuCysProCysArgGlnGluHisIleGly 1070
Db 3618 ACCTCAGCTCGCGCGCCCTACTCTCTGCT-GCCTGTGTGTGCTCTGGGGGTACTGCCCA 3676
Qy 1071 MetProMetAsnThrPro 1076
Db 3677 ACTCTCGGTGACACCA 3694

RESULT 5
AAS01433
ID AAS01433 standard; cDNA; 3339 BP.
XX
AC AAS01433;
XX
XX 04-JUL-2001 (first entry)
XX
DE Human secreted soluble alpha2delta calcium channel subunit #18 cDNA.
XX
XX Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;
KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;
KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;
KW filter binding assay; wheat germ lectin flashplate assay; ss.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT CDS 3..3339
FT /partial
FT /product= "Alpha2delta calcium channel subunit #18"
FT /note= "this sequence lacks a stop codon"
FT /transl_except= (pos:2241..2246,aa:Ala-Ser-Gly)
FT /note= "These codons have an apparent 3 nucleotide
FT deletion"
FT /transl_except= (pos:2286..2340,aa:Ser-Asp)
FT /note= "These two codons between them have an apparent 49
FT nucleotide insertion which alters the reading frame"
XX
XX WO200119870-A2.
XX
XX 22-MAR-2001.
XX
XX 18-SEP-2000; 2000WO-EP009137.
XX
XX 16-SEP-1999; 99US-00397550.
XX
XX (WARN ) WARNER LAMBERT CO.
XX
XX Brown JP, Bertelli F;
XX
XX WPI; 2001-235262/24.
XX
XX P-PSDB; AAU01038.
XX
XX Calcium channel alpha2delta subunits, useful in e.g. SPA assays,
XX Flashplate assays, Nickel Flashplate assays, Filter binding assays or
XX Wheat Germ Lectin Flashplate assays.
XX
XX Claim 39; Page 148-149; 160pp; English.
XX
XX The present sequence encodes for human secreted calcium channel
XX alpha2delta subunit #18 which is soluble and retains the functional
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Qy 591 GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu 610
Db 1914 GGCCACGAGAAATACATCTTCTGGGAAACACGCTGTGGAAAGAGCGCTGCATGACTTG 1973
Qy 611 LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630
Db 1974 CTTCCACCAGACCTTGGCCCTTGGCCGAGTGTGATCTACTGCATCACAGATATTGACCCA 2033
Qy 631 AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro 650
Db 2034 GACCACCGAAGCTCAGCAGCTAGAGCCATGATCCGCTTCCTCACCAGGAAGACCCA 2093
Qy 651 AspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValThrAla 670
Db 2094 GACCTGAGTGTGACGAGGAGCTGCTCGGAGGTGCTGTTTGACGGCGTGTGACAGCC 2153
Qy 671 ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisVal 690
Db 2154 CCNATGGAAGCCTACTGGACAGCGCTGGCCCTCAACATGTCCGAGGAGTCTGAACACGTG 2213
Qy 691 ValAspMetAlaPheLeuGlyThrArgAla----- 700
Db 2214 GTGACATGCGCTTCTTGGGACCCCGGCTGGCCCTCTGAGAACGAGCTTGTTCGTGGGC 2273
Qy 701 -----GlyLeuLeuArgSerSerLeuPheValGlySerGluLysVa 714
Db 2274 TCCGAGAAGGTCTCCGAGTGGCCCTCTCAGAAAGCAGCTTGTTCGTGGGCTCCGAGAAGGT 2333
Qy 714 lSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeuAspArgPh 734
Db 2334 CTTCCGACGAAGTTCCTGACACCTGAGGACGAGCGCAGCGTGTTCACCTTGGACCGCTT 2393
Qy 734 eProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheValPheAsnLeuAr 754
Db 2394 CCGCTGTGTACCGCCAGGCCCTCAGAGCATCTCTGCTGGCAGCTTCTCTTCAACCTCCG 2453
Qy 754 gTrpAlaGluProGluSerAlaGlyGluProMetValValThrAlaSerThrAlaVa 774
Db 2454 CTGGCAGAAAGGACAGAAAGTGGCGGTGAACCCATGCTGTGACGCGCAAGCAGAGTGT 2513
Qy 774 lAlaValThrValAspLysArgThrAlaIleAlaAlaAlaGlyValGlnMetLysLe 794
Db 2514 GCGGTGACCTGGACAAAGGACAGCCATTTCTGCAGCGCCGCGGCGTCCAAATGAAGCT 2573
Qy 794 uGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThrValAspGlyPr 814
Db 2574 GGAATTCCTCCAGCGCAAAATCTGGCGGCAACCGCGCAGTCGACACTGTGGATGGGCC 2633
Qy 814 oTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAspAsnAsnGlyPh 834
Db 2634 GTGCACACAGAGCTGCCGAGGACAGTGATCTGGACTGCTGATCGACAAACAACGCGGTT 2693
Qy 834 eIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyValValAspGlyAl 854
Db 2694 CATTCGATCTCCAAAGAGTCCCGAGAGACGGGAAGATTTCTGGGGAGGTGGAATGGTC 2753
Qy 854 aValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMetTyrAspTyrGl 874
Db 2754 TGTCTCTGACCGAGCTGCTCAGCATGGGGGTGTTTCAGCCCAAGTGACTATGATGACTATCA 2813
Qy 874 nAlaMetCysLysProSerSerHisHisHisSerAlaAlaGlnProLeuValSerProIl 894
Db 2814 GGCCATGTGAAACCCCTCGAGTCACCAACCAAGTCAGTCAGCCAGCCCTGGTGCAGCCCAAT 2873
Qy 894 eSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuGlu 914
Db 2874 TTCGCTCTTTCAGCGGACCGAGGTGGCTGCTGCAGAGCTGGTGTGTTCTTCGTGGA 2933
Qy 914 uTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSerValPheHisHi 934
Db 2934 GTGGAGTGTCTGGGGCTCTCTGGTACGACAGAGGGCGGAGCCAAAGTGTCTTCCATCA 2993
Qy 934 sSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrProValPh 954

Db 2994 CTCCCAAAACACAAGAGCAGGACCCGCTGCAGCCCTGCACACGAGTAGTACCCTGTT 3053
Qy 954 eValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLy 974
Db 3054 CGTGTACCAACCGCCCATCCGGAGGCCAACGGGATCTGTGAGTGCGGGCTCCAGAA 3113
Qy 974 sValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuValThrAspProTh 994
Db 3114 GGTATTGTGGTGAGCAGATTCCTCCAAACAGTAACTCTCTCTCTGCTGACAGACCCAC 3173
Qy 994 rCysAspCysSerIlePheProValLeuGlnGluAlaThrGluValLysTyrAsnAl 1014
Db 3174 CTGTGACTGCAGCATCTTCCACCATGCTGCAGAGGCGCAGAAAGTCAAAATAATATGC 3233
Qy 1014 aSerValLysCysAspArgMetArgSerGlnLysLeuArgArgProAspSerCysHi 1034
Db 3234 CTCTGTCAATGTGACCGGATCGCTCCAGAGCTCCGCGGCGGACGACTCTTGCCA 3293
Qy 1034 sAlaPheHisProGluValArgValGluAlaAspArgGlyTrpAla 1049
Db 3294 CGCTTCCATCCAGAGGAGAAATGCCAG---GACTGCGCGGCGCC 3336
RESULT 6
AAFS7570
ID AAFS7570 standard; DNA; 3339 BP.
XX
AC AAFS7570;
XX
DT 11-JUN-2001 (first entry)
XX
DE Human calcium channel alpha2delta subunit encoding DNA.
XX
KW Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;
KW nervous system disorder; pain; epilepsy; anxiety; human; ds.
XX
OS Homo sapiens.
XX
PN WO200120336-A2.
XX
PD 22-MAR-2001.
XX
PF 18-SEP-2000; 2000WO-EP009136.
XX
PR 16-SEP-1999; 99US-00397549.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;
XX
DR WPI; 2001-257902/26.
XX
PT Competitive binding assay for screening ligands which bind a cerebral
cortical voltage-dependent calcium channel alpha2-delta-1 subunit, where
the ligands identified are useful for treating disorders of the nervous
system, including pain.
XX
PS Disclosure; Page 146-147; 158pp; English.
XX
CC The invention relates to a new method for screening ligands which bind a
cerebral cortical voltage-dependent calcium channel alpha2delta subunit,
preferably alpha2delta-1 subunit. The method comprises contacting a
secreted soluble recombinant alpha2delta-1 subunit with a ligand of
interest and a labelled compound which binds the subunit, followed by
measuring the level of binding of the labelled compound to alpha2delta-1
subunit. The method is useful for screening ligands, preferably
biologically active products that modulate a nervous system function,
which bind a cerebral cortical voltage-dependent calcium channel
alpha2delta-1 subunit. The ligands identified by the method are useful
for treating disorders of the nervous system, including pain, epilepsy
and anxiety. The present sequence represents a human calcium channel
alpha2delta subunit encoding DNA
XX

SQ	Sequence	3339 BP; 780 A; 934 C; 960 G; 665 T; 0 U; 0 Other;
Alignment Scores:		
Pred. No.:	0	Length: 3339
Score:	5342.50	Matches: 1028
Percent Similarity:	97.54%	Conservative: 2
Best Local Similarity:	97.35%	Mismatches: 8
Query Match:	93.30%	Indels: 18
DB:	5	Gaps: 2
US-09-833-222A-10 (1-1090) x AAF57570 (1-3339)		
Qy	11	AspArgValLysLeuTrpAlaAspThrPheGlyAspLeuTrpAsnThrValThrLys 30
Db	174	GAACAGTGAAGCTATGGCTGACACCTTCGGCGGGACCTGTATAACACTGTGACCAA 233
Qy	31	TyrSerGlySerLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
Db	234	TACTCAGGCTCTCTTGTCTGCAGAAAGTACAAAGATGTGGAGTCCAGTCTGAAGATC 293
Qy	51	GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
Db	294	GAGAGGTGGATGCTTGGAGCTGGTGGAGAGTTCTCAGAGCATGGAGACATGCTG 353
Qy	71	ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluAlaAspLeuAsn 90
Db	354	CGGAGGAAAGTCGAGGCGGTCAGAACTCTGTGGAAGCTGCCGAGGAGCGGACCTGAAC 413
Qy	91	HisGluPheAsnGluSerLeuValPheAspTyrTrpAsnSerValLeuIleAsnGluArg 110
Db	414	CACGAATTCGAATGAATCCCTGGTGTTCGACTATTACAACTCGGTCTTGATCAACGAGAG 473
Qy	111	AspGluLysGlyAsnPheValGluLeuGlyValadGluPheLeuLeuGluSerAsnAlaHis 130
Db	474	GACGAGAAGGCAACTTCGTGGAGCTGGGCGCGAGTTCTCTGGAGTCCAATGTCTAC 533
Qy	131	PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr 150
Db	534	TTCAGCAACCTGCGCGGTGAACACCTCCATCAGCAGCGTCGAGCTGCCACCAACGTTGAC 593
Qy	151	AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe 170
Db	594	AACAAAGACCCAGATATTTAAATGGAGTCTACATGTCGAAGCTTGAATGTCTTCTTC 653
Qy	171	ValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGly 190
Db	654	GTGGAGAACTTCNAGAGACCCACAGCTTGACCTGGCAATATTTGGCAGTGCACATGGA 713
Qy	191	PhePheArgIleTyrProGlyIleLysTrpThrProAspGluAsnGlyValIleThrPhe 210
Db	714	TTCTTCAGGATCTATCCAGGTATAAAATGGACACCTGATGAGAATGGAGTCAATTAATTTT 773
Qy	211	AspCysArgAsnArgGlyTrpTyrIleGluAlaThrSerProLysAspIleValIle 230
Db	774	GACTGCCGAACCGCGCTGGTACATTCAAAGCTGCTACTTCTCCCAAGGACATAGTGATT 833
Qy	231	LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle 250
Db	834	TTGGTGGACGTGAGCGCATGTGAAGGGGCTGAGGATGACTATTGCCAAGCACACCAATC 893
Qy	251	ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp 270
Db	894	ACCACCATCTTGGACACCTTGGGGAGAAATGACTTCGTGTTAATATATAGGCTACAATGAC 953
Qy	271	TyrValHisTyrIleGluProCysPheLysGlyLeuValGlnAlaAspArgAspAsn 290
Db	954	TACGTCCATTACATCGAGCTTGTTTTAAAGGATCCTCGTCAGCGCGGACCGAGACAAT 1013
Qy	291	ArgGluHisPheLysLeuLeuValGluLeuMetValLysGlyValGlyValValAsp 310
Db	1014	CGAGAGCATTTCAAATCTGCTGGAGAGTTCATGGTCAAAAGTGTGGGGTCTGTGGAC 1073
Qy	311	GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer 330
Db	1074	CAAGCCCTGAGAGAAGCCTTCCAGATCTCTGAAGCAGTTCTCAAGAGGCCAAGGAAGC 1133
Qy	331	LeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal 350
Db	1134	CTCTGCAACACAGGCCCATCATGTCTCAGCGAGCGCGCGTGGAGACTACAGACCGGTG 1193
Qy	351	PheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArg 370
Db	1194	TTTGAGAGTATTAACCTGGCCAGACTGTAAAGTCCGAGTTTCTACTACCTCATTTGGAGA 1253
Qy	371	GluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThr 390
Db	1254	GAAGTGTCTTTTCTGACCGCATGAAGTGGATTGCATGCACAACAAGAGGCTACTACACG 1313
Qy	391	GlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer 410
Db	1314	CAGATCTCAACGCTGGCGGACACCCAGGAGAACGTGATGGAATACCTGCACGTGCTCAGC 1373
Qy	411	ArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSer 430
Db	1374	CGCCCCATGGTCAATCAACCGACACGACATCATCTGGACAGAGGCTTACATGGACAGC 1433
Qy	431	LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProVal 450
Db	1434	AGCTCTCAGCTCGCAGGCTCAGAGCCTGACACTGCTCACACTGTGGCCATGCCAGTTC 1493
Qy	451	PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp 470
Db	1494	TTCAGCAAGAAAGAACCAAAACCGGATCCCATGGCATTTCTCTGGGTGTGGTGGCTCAGAT 1553
Qy	471	ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr 490
Db	1554	GTGGCCCTGAGAGAGCTGATGAAGCTGGCGCCCCGGTACAAGCTTGGAGTGCACGGATAC 1613
Qy	491	AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr 510
Db	1614	GCCTTTCTGAACACCAACCAATGGCTACATCTCTCCCATCCCGACCTCCGCGCCCTGTAC 1673
Qy	511	ArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal 530
Db	1674	AGAGGGGGAAGAAATCAAAACCCAAACCTAACTACAAACAGTGTGGATCTCTCCGAAGTG 1733
Qy	531	GluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
Db	1734	GAGTGGAGAACCGGCTGAATCTCTGAGAACAGCCATCATCAATAGGAGAACAGGTACT 1793
Qy	551	LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570
Db	1794	CTCTCGATGGATGTGAAGGTTCCGATGGATATAAGGGAAGCGAGTTCTTTTCTGTGACCAAT 1853
Qy	571	AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
Db	1854	GACTACTCTTTCACGGACATCAGCACACCTTTTTCAGTTTGGGGGTGGTGTCTCCCGG 1913
Qy	591	GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu 610
Db	1914	GGCCACGGAGATACATCTTCTGGGAACACGCTGTGTGGAGAGGCCCTGCATGACTTG 1973
Qy	611	LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630
Db	1974	CTTCAACCCAGACCTGGCCCTGGCGGTGACTGGATCTACTGCATCATCAGATATTGACCCA 2033
Qy	631	AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro 650
Db	2034	GACCCCGGAAGCTCAGCAGCTAGAGGCCATGATCCGCTTCTCTACCCAGGAGGACCCA 2093
Qy	651	AspLeuGluCysAspGluLeuValArgGluValLeuPheAspAlaValValThrAla 670
Db	2094	GACCTGGAGTGTGACGAGGAGCTGGTCCGGGAGGTGCTCTTTGACCGGTGGTGACAGCC 2153
Qy	671	ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisVal 690

Db 2154 CCCATGGAAGCCTACTGACACAGCCCTGGCCCTCAACATGTCCGAGGAGTCTGAAACAGTG 2213
Qy 691 ValAspMetAlaPheLeuGlyThrArgAla----- 700
Db 2214 GTGGACATGGCTTCTCTGGGCACCCGGCTGGCCCTCCTGAGAACGAGCTTGTTCGTGGGC 2273
Qy 701 -----GlyLeuLeuAtrgSerSerLeuPheValGlySerGluLysVa 714
Db 2274 TCCGAGAAGGTCTCCGAGTGGCCCTCTGAGAAGCAGCTTGTTCGTGGGC 2333
Qy 714 lSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeuAspArgPh 734
Db 2334 CTCCGACAGGAAGTCTCTGACACCTGAGGACGAGCCAGCTGTTCACCTGGACCCGCTT 2393
Qy 734 eProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheValPheAsnLeuAr 754
Db 2394 CCCGCTGTGGTACCGCCAGGCTCAGAGCATCTCTGCTGGCAGCTTCTTCAACCTCCG 2453
Qy 754 gTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAlaSerThrAlaVa 774
Db 2454 CTGGGCAGAGGACAGAAAGTGGCGGTGAACCCATCGTGGTGCACGGCAAGCAGAGCTGT 2513
Qy 774 lAlaValThrValAspLysArgThrAlaIleAlaAlaAlaGlyValGlnMetLysLe 794
Db 2514 GCGCGTGACCGTGACAGAGGACAGCCATTTGTCAGCCGCGGGCGTCCAAATGAAGCT 2573
Qy 794 uGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThrValAspGlyPr 814
Db 2574 GGAATTCCTCCAGCGCAATTCCTGGCGGCAACCGGCGAGTGCAGACACTGTGGATGGCC 2633
Qy 814 oTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAspAsnGlyPh 834
Db 2634 GTGCACACAGAGCTGCGAGGACAGTGATCTGGACTGTCTGTCATCGACACACACGGGTT 2693
Qy 834 eIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGluValAspGlyAl 854
Db 2694 CATTCGTATCTCCAAGAGGTCCCGAGAGACGGGAAGATTTCTGGGGGAGGTGGATGTGC 2753
Qy 854 aValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMetTyrAspTyrGl 874
Db 2754 TGTCTGACCCAGCTGCTCAGCATGGGGTGTTCAGCCAAAGTGACTATGATGACTATCA 2813
Qy 874 nAlaMetCysLysProSerSerHisHisSerAlaAlaGlnProLeuValSerProIl 894
Db 2814 GGCCATGTGAAACCTCGAGTCAACACAGTGCAGCCAGCCCGCTGTGTGACGCCAAT 2873
Qy 894 eSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLeuGl 914
Db 2874 TTTGCGCTTCTTGACGGCGACCAAGTGGCTGCTCGAGAGCTGTGTCTCTCTCTGGGA 2933
Qy 914 uTrpSerValTrpGlySerTrpTyrAspArgGlyValAlaGluAlaLysSerValPheHisH 934
Db 2934 GTGGAGTGTCTGGGGCTCTGTTAGCAGACAGAGGGCGGCGGCAAAAGTGTCTTCCATCA 2993
Qy 934 sSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrProValPh 954
Db 2994 CTCCCAACAAACACAGAAGCAGGACCGCGCTGCAGCCCTGCGACACGAGTACCCCGTGT 3053
Qy 954 eValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLy 974
Db 3054 CGTGTACCGCGGCCCATCCGGAGGCCAACGGGATCGTGGAGTGGCGGGCCCTGCCAGAA 3113
Qy 974 sValPheValValGlnGlnProAsnSerAsnLeuLeuLeuValThrAspProTh 994
Db 3114 GGTATTGTGTGGTGCAGCAGATTCCCAACAGTAACTCTCTCTCTGTGTGACAGACCCAC 3173
Qy 994 rCysAspCysSerIlePheProValLeuGlnGluAlaThrGluValLysTyrAsnAl 1014
Db 3174 CTGTGACTGCAGCATCTTCCACCAAGTGTGTGCAGGAGCGCAGAGTCAAAATAATGC 3233
Qy 1014 aSerValLysCysAspArgMetArgSerGlnLysLeuLeuArgProAspSerCysHi 1034
Db 3234 CTCTGTCAAAATGTACCGGATGCCCTCCAGAAAGCTCCGCGGGGACAGACTCTCTGCCA 3293

Qy 1034 sAlaPheHisProGluValArgValGluAlaAspArgGlyTrpAla 1049
Db 3294 CGCTTCCATCCAGAGGAGAAATGCCAG---GACTGGCGGGCGCC 3336

RESULT 7

AAS01432
ID AAS01432 standard; cDNA; 3209 BP.

XX AC AAS01432;

XX DT 04-JUL-2001 (first entry)

XX DE Human secreted soluble alpha2delta calcium channel subunit #17 cDNA.

XX KW Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;
KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;
KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;
KW filter binding assay; wheat germ lectin flashplate assay; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 3...3209

XX FT /partial

XX FT /product= "Alpha2delta calcium channel subunit #17"

XX FT /note= "This sequence lacks a stop codon"

XX PN W0200119870-A2.

XX PD 22-MAR-2001.

XX PP 18-SEP-2000; 2000MO-EP009137.

XX PR 16-SEP-1999; 99US-00397550.

XX PA (WARN) WARNER LAMBERT CO.

XX PI Brown JP, Bertelli F;

XX PPI; 2001-235262/24.

XX P-PSDB; AAU01037.

XX CC Calcium channel alpha2delta subunits, useful in e.g. SPA assays,
XX Flashplate assays, Nickel Flashplate assays, Filter binding assays or
XX Wheat Germ Lectin Flashplate assays.

XX PS Claim 39; Page 147-148; 160pp; English.

XX CC The present sequence encodes for human secreted calcium channel
XX alpha2delta subunit #17 which is soluble and retains the functional
XX characteristics of the full length or wild type alpha2delta subunit
XX (AAU01025) from which it is derived. The invention relates to truncated
XX alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins
XX which retain their affinity for radioactively labelled gabapentin. The
XX alpha2delta subunit is 1 of the components of the heteromultimeric
XX voltage-dependent calcium channel (VDCC) complexes present in neuronal
XX and non-neuronal tissues including heart and skeletal muscle. Numerous
XX soluble forms of the human calcium channel alpha2delta subunits (AAU01014
XX -AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the porcine
XX calcium channel alpha2delta subunits (AAU01027-AAU01031) are described.
XX The secreted soluble alpha2delta subunit may be used in assays e.g.
XX scintillation proximity assay (SPA), flashplate, nickel flashplate,
XX filter binding or wheat germ lectin flashplate assays to detect or
XX measure the binding or interaction of a ligand (e.g. gabapentin, L-
XX Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine, L-
XX Valine, Spermine and/or L-Phenylalanine) of a calcium channel alpha2delta
XX subunit

XX SQ Sequence 3209 BP; 757 A; 888 C; 920 G; 644 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0
Score: 5276.00
Percent Similarity: 99.70%
Best Local Similarity: 99.60%
Query Match: 92.14%
DB: 4
Gaps: 0

US-09-833-222A-10 (1-1090) x AAS01432 (1-3209)

QY	11	AspArgValLysLeuTrpAlaAspThrPheGlyAspLeuTyrAenThrValThrLys	30
DB	174	GAACAGTGAAGCTATGGCTGACACCTTCGGGGGACCTGTATACACTGTGACCAA	233
QY	31	TyrSerGlySerLeuLeuGlnLysLysLysLysLysLysLysLysLysLysLys	50
DB	234	TACTCAGGCTCTCTCTGCTGCAAGAGTACCAAGATGTGAGTCCAGTCTGAAGATC	293
QY	51	GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAenMetLeu	70
DB	294	GAGGAGTGGATGGCTTGGAGCTGGTGAGGAAGTTCTCAGAGACATGGAGAACATGCTG	353
QY	71	ArgArgLysValGluAlaValGlnAenLeuValGluAlaGluAlaAspLeuAen	90
DB	354	CGAGGAAAGCTCAGGCGGTCCAGAACTCTGCTGGAAGCTGCCGAGGAGCGCCACTGAAC	413
QY	91	HisGluPheAenGluSerLeuValPheAspTyrTyrAenSerValLeuLysLysLysLys	110
DB	414	CACGAATTCATGAATCCCTGGTGTTCGACTATTACAACTCGGTCTGATCAACGAGAGG	473
QY	111	AspGluLysGlyAenPheValGluLeuGlyAlaGluPheLeuLeuGluSerAenAlaHis	130
DB	474	GACGAGAGGCAACTTTCGTGGAGCTGGGCGCGAGTTCTCTCGTGGATCCAAATGCTCAC	533
QY	131	PheSerAenLeuProValAenThrSerIleSerSerValGlnLeuProThrAenValTyr	150
DB	534	TTCAGCAACCTGCGGTGAACCTCCATCAGCAGCGTGCAGCTGCCACCAACGCTGTAC	593
QY	151	AsnLysAspProAspLysLeuAenGlyValTyrMetSerGluAlaLeuAenAlaValPhe	170
DB	594	AACAAGACCCAGATATTTAAATGGAGTCTACATGTCGAAGCTTGAATGCTGCTTC	653
QY	171	ValGluAenPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGly	190
DB	654	GTGGAGAACTTCCAGAGAGACCCAAACGTTGACCTGGCAATATTTGGCAGTGCACCTGGA	713
QY	191	PhePheArgLysTyrProGlyLysLysLysLysLysLysLysLysLysLysLysLys	210
DB	714	TTCTTCAGGATCTATCCAGGTATATAATGGACACCTGATGAGAAATGGAGTCAATTACTTTT	773
QY	211	AspCysArgAenArgGlyTyrTyrIleGlnAlaAlaThrSerProLysAspLysLysLys	230
DB	774	GATCGCCAAACCGCGCTGTTATCATTTCAAGCTGCTACTTCTCCCAAGGACATAGTATT	833
QY	231	LeuValAspValSerGlySerMetLysGlyLeuArgMetThrLysLysLysLysLysLys	250
DB	834	TTGGTGGACGTGAGCGGCAGTATGAGGGGCTGAGGATGACTATTGCCAAGCACACCATC	893
QY	251	ThrThrLysLeuAspThrLeuGlyGluAenAspPheValAenLysLysLysLysLysLys	270
DB	894	ACCACCATCTTGGACACCTTGGGGGAGAAATGACTTCGTTAATATCATAGCGTCAATGAC	953
QY	271	TyrValHisTyrIleGluProCysPheLysGlyLysLysLysLysLysLysLysLysLys	290
DB	954	TAGTTCATATCATCGAGCTTGTGTTAAAGGAGTCTCTCGTCAGGGCGGACCGAGACAT	1013
QY	291	ArgGluHisPheLysLeuValGluLeuMetValLysGlyValGlyValValAsp	310
DB	1014	CGAGAGCATTTCAAACTGCTGGTGGAGAGTTCATGCTCAAAAGTGTGGGGGCTCGTGGAC	1073
QY	311	GlnAlaLeuArgGluAlaPheGlnIleLysGlnPheGlnGlnLysLysLysLysLysLys	330
DB	1074	CAAGCCCTGAGAGAGCTTCCAGATCTTCAAGCAGTTCCAAAGGCGCAAGCAAGGAAC	1133

QY	331	LeuCysAenGlnAlaIleMetLeuLysSerAspGlyAlaValGluAspTyrGluProVal	350
DB	1134	CTCTGCAACAGGCGCATCATGCTCATCAGGAGCGCGCTGGAGGACTACAGAGCGGTG	1193
QY	351	PheGluLysTyrAenTrpProAspCysLysValArgValPheThrTyrLeuLysGlyArg	370
DB	1194	TTTGAGAGTATATAACTGGCCAGACTGTAAAGTCCGAGTTTTCCTTACCTCAITGGGAGA	1253
QY	371	GluValSerPheAlaAspArgMetLysTrpIleAlaCysAenAenLysGlyTyrTyrThr	390
DB	1254	GAAGTGTCTTTTGTCTGACCGCATGAAGTGGATTCATGCAACCAACAAAGGCTACTACAG	1313
QY	391	GlnIleSerThrLeuAlaAspThrGlnGluAenValMetGluTyrLeuHisValLeuSer	410
DB	1314	CAGATCTCAACGCTGGCGGACACCCAGGAGAACTGATGGAATACCTGCACGCTGCTCAGC	1373
QY	411	ArgProMetValIleAenHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSer	430
DB	1374	CGCCCCATGTCATCAACCAACGACCGACATCATCTGGACAGAGGCTTACATGGACAGC	1433
QY	431	LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProVal	450
DB	1434	AAGCTCTCAGCTCGCAGGCTCAGACCTGACACTGCTACCACTGTGGCCATGCCAGTC	1493
QY	451	PheSerLysLysAenGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp	470
DB	1494	TTCAGCAAGAAAGAACCGCATCCCATGGCATTTCTCTGGGTGTGGTGGCTCAGAT	1553
QY	471	ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr	490
DB	1554	GTGGCCTCAGAGAGCTGATGAAGCTGGCGCCCGGTACAAGCTTGGAGTGCACGGATAC	1613
QY	491	AlaPheLeuAenThrAenAenGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr	510
DB	1614	GCCTTTCTGAACACCAACCAATGGCTACATCTCTCCCATCCCCGACCTCCGGCCCTGTAC	1673
QY	511	ArgGluGlyLysLysLeuLysProLysProAenTyrAenSerValAspLeuSerGluVal	530
DB	1674	AGGAGGGGAAAGAACTTAAACCCAACTAACAACAGCTGGATCTCTCCGAAGTG	1733
QY	531	GluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAenArgGluThrGlyThr	550
DB	1734	GAGTGGAAAGACCCAGGCTGAATCTCTGAGAAACCACTGATCAATAGGGAACAGGTACT	1793
QY	551	LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn	570
DB	1794	CTCTCATGATGTGAAGGTTCCGATGGATAAAGGAAGCGAGTTCTTTTCTTGACCAAT	1853
QY	571	AspTyrPhePheThrAspLysSerAspThrProPheSerLeuGlyAlaValLeuSerArg	590
DB	1854	GACTACTTCTTACCGACATCAGCGACACCCCTTTTTCAGTTTGGGGTGGTGTCTCCCGG	1913
QY	591	GlyHisGlyGluTyrIleLeuLeuGlyAenThrSerValGluGluGlyLeuHisAspLeu	610
DB	1914	GGCCACGGAGAAATACATCTCTTGGGGGACACGCTCTGTGGAAGAAGGCGCTGATGACTG	1973
QY	611	LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro	630
DB	1974	CTTACCCACAGACTGGCCCTGGCGGTGACTGGATCTTACTGCAATCACAGATATTGACCCA	2033
QY	631	AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro	650
DB	2034	GACCACCGGAAGCTCAGCCAGCTAGAGGCCATGATCCGCTTCTCTACCAAGGAAGGCCCA	2093
QY	651	AspLeuGluCysAspGluLeuValArgGluValLeuPheAspAlaValValThrAla	670
DB	2094	GACCTGGAGTGAACAGGAGCTGGTCCGGAGGTGCTGTTTTCACCGGTGGTGACAGCC	2153
QY	671	ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAenMetSerGluGluSerGluHisVal	690
DB	2154	CCCATGGAGGCTTACTGGACAGGCTGGCCCTCAACATGTCGCGGAGGTCTGGAACAGTG	2213
QY	691	ValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGly	710

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Db 2214 GTGACATGGCTTCCTGGGACCCGGCTGGCCCTCTCTGAGAACGAGCTTGTTCGTGGGC 2273
Qy SerGluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThr 730
Db 2274 TCCGAGAAAGTCTCCGACAGGAAGTTCTGACACTGAGGACGAGGCGAGGTTTCAACC 2333
Qy LeuAspArgPheProLeuThrPheArgGlnAlaSerGluHisProAlaGlySerPheVal 750
Db 2334 CTGGACCGCTTCCCGCTGTGGTACCGCGAGGCTCAGACATCTCTGTGGCAGCTTCGTC 2393
Qy PheAsnLeuArgTTPAlaGluGlyProGluSerAlaGlyGluProMetValValThrAla 770
Db 2394 TTCAACCTCCGCTGGGCGAGAGGACCAAGAAAGTCCGGGTGAACCATGGTGGTACCGGCA 2453
Qy SerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaGlyVal 790
Db 2454 AGCACAGCTGGGGGTGGGCGTGGACAGAGGACAGCCATTGTCTGACGCGGGGCTC 2513
Qy GlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThr 810
Db 2514 CAAATGAAGCTGGAATTCCTCAGCGCAAAATTCCTGGCGGCAACGCGCAGTCAGCACT 2573
Qy ValAspGlyProThrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAsp 830
Db 2574 GTGGATGGCGCGTGCACACAGAGCTGCGAGGACAGTGATCTGGACTGCTTCGTCTCATCGAC 2633
Qy AsnAsnGlyPheIleLeuLeuSerLysArgSerArgGluThrGlyArgPheLeuGlyGlu 850
Db 2634 AACAAACGGTTCATCTCTGATCTCCAGAGGTCCCGAGAGCGGGAAGATTTCTGGGGAG 2693
Qy ValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMet 870
Db 2694 GTGGATGGTGTCTCTGACCCAGCTGCTCAGCATGGGGTGTTCAGCCAAAGTGAATG 2753
Qy TyrAspTyrGlnAlaMetCysLysProSerSerHisHisSerAlaAlaGlnProLeu 890
Db 2754 TATGACTATCAGGCGCATGTGCAAACTTCGAGTCCACCACACAGTGCAGCGCCAGCCCTG 2813
Qy ValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeu 910
Db 2814 GTACGCCCAATTTCTGCTTCTTGACCGGCAGCCAGTGGTCTGTCAGGAGCTGGTCTG 2873
Qy PheLeuLeuGluTrpSerValTrpGlySerTrpTrpAspArgGlyAlaGluAlaLysSer 930
Db 2874 TTCCTGTGGAGTGGAGTGTCTGGGCTCTCTGTGTACGACAGAGGGGCGGAGGCCAAAGT 2933
Qy ValPheHisSerHisLysHisLysGlnAspProLeuGlnProCysAspThrGlu 950
Db 2934 GTCTTTCATCACTCCCAACAACAAGAGCAGGACCCGCTGCGAGCCCTCGCACCGGAG 2993
Qy TyrProValPheValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGly 970
Db 2994 TACCCCTGTGTGTACACAGCGGCCCATCCGGAGAGCCCAACGGGATCTGGAGTGGCGG 3053
Qy ProCysGlnLysValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuVal 990
Db 3054 CCCTGCCAGAGGATTTGTGTGTGTCAGCAGATTCCTCCCAACAGTAACTCTCTCTCTG 3113
Qy ThrAspProThrCysAspCysSerIlePheProProValLeuGlnGluAlaThrGluVal 1010
Db 3114 ACAGACCCCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3173
Qy LysTyrAsnAlaSerValLysCysAspArgMetArg 1022
Db 3174 AATATATAGTCCCTCTGTCAAAATGTGACCGGATGGCC 3209
RESULT 8
AAF57569
ID AAF57569 standard; DNA; 3209 BP.
XX
AC AAF57569;
XX
```

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DT 11-JUN-2001 (first entry)
XX Human calcium channel alpha2delta subunit encoding DNA.
DE
XX Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;
KW nervous system disorder; pain; epilepsy; anxiety; human; de.
XX Homo sapiens.
XX OS
XX Key Location/Qualifiers
PH CDS 3..3209
FT /*tag= a
XX
XX WO200120336-A2.
XX
XX 22-MAR-2001.
XX
XX 18-SEP-2000; 2000WO-EP009136.
XX
XX 16-SEP-1999; 99US-00397549.
XX (WARN ) WARNER LAMBERT CO.
XX
XX Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;
XX WPI; 2001-257902/26.
XX P-PSDB; AAB62261.
XX
XX Competitive binding assay for screening ligands which bind a cerebral
XX cortical voltage-dependent calcium channel alpha2-delta-1 subunit, where
XX the ligands identified are useful for treating disorders of the nervous
XX system, including pain.
XX
XX Disclosure; Page 145-146; 158pp; English.
XX
XX The invention relates to a new method for screening ligands which bind a
XX cerebral cortical voltage-dependent calcium channel alpha2delta subunit,
XX preferably alpha2delta-1 subunit. The method comprises contacting a
XX secreted soluble recombinant alpha2delta-1 subunit with a ligand of
XX interest and a labelled compound which binds the subunit, followed by
XX measuring the level of binding of the labelled compound to alpha2delta-1
XX subunit. The method is useful for screening ligands, preferably
XX biologically active products that modulate a nervous system function,
XX which bind a cerebral cortical voltage-dependent calcium channel
XX alpha2delta-1 subunit. The ligands identified by the method are useful
XX for treating disorders of the nervous system, including pain, epilepsy
XX and anxiety. The present sequence represents a human calcium channel
XX alpha2delta subunit encoding DNA
XX
XX Sequence 3209 BP; 757 A; 888 C; 920 G; 644 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 0 Length: 3209
Score: 5276.00 Matches: 1008
Percent Similarity: 99.70% Conservative: 1
Best Local Similarity: 99.60% Mismatches: 3
Query Match: 92.14% Indels: 0
DB: 5 Gaps: 0
US-09-833-222a-10 (1-1090) x AAF57569 (1-3209)
Qy 11 AspArgValLysLeuTrpAlaAspThrPheGlyAspLeuTyrAsnThrValThrLys 30
Db 174 GAAACAGTGAAGCTATGGCTGACACCTTCGGCGGGGACCTGTATACACTGTGACCAA 233
Qy 31 TyrSerGlySerLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
Db 234 TACTCAGGCTCTCTCTTGTCTGCAGAGAAAGTACAAGATGTGGAGTCCAGTCTGGAAGATC 293
Qy 51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
Db 294 GAGGAGTGGATGGCTTGGAGCTTGGAGCTGGTGGAGGAAGTTCTCAGAGGACATGGAGACATGCTG 353
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Qy	71	Arg	Gly	Ser	Val	Glu	Ala	Val	Ile	Asn	Leu	Val	Glu	Ala	Ala	Glu	Ala	Asp	Leu	Asn	90
Db	354	CGG	AGG	AAAGT	CGAGG	CGGT	CCAGAA	TCTGGT	GGAAGCTG	CCGAGGAGG	CGCCG	ACTGAAC	413								
Qy	91	His	Glu	Phe	Asn	Glu	Ser	Leu	Val	Phe	Asp	Tyr	Tyr	Asn	Ser	Val	Leu	Ile	Asn	Glu	Arg
Db	414	CAC	GAA	TTT	CAAT	GAAAT	CCCTGGT	TTCGACT	TATTTACAACT	CGGTCCG	TGATCAAC	GAAGG	473								
Qy	111	Asp	Glu	Leu	Ser	Gly	Asn	Phe	Val	Glu	Val	Ala	Glu	Phe	Leu	Leu	Glu	Ser	Asn	Ala	His
Db	474	GAC	GAG	AAAGG	CAACT	TCGTGGAGCT	GGGCGCC	GAGTTCTCT	CTGGAGATCC	AAATGCTCT	GAATGCTGTCTTC	653									
Qy	131	Phe	Ser	Asn	Leu	Pro	Val	Asn	Thr	Ser	Ile	Ser	Ser	Val	Gln	Leu	Pro	Thr	Asn	Val	Tyr
Db	534	TTT	CAGCAAC	CTGCCG	TGAAACAC	CTCCATCAG	CAGCGTGCAGCT	GTGCC	CAACCACTG	TGATCAAC	CACTGTGATC	593									
Qy	151	Asn	Leu	Ser	Pro	Asp	Ile	Leu	Asn	Gly	Val	Tyr	Met	Ser	Glu	Ala	Leu	Asn	Ala	Val	Phe
Db	594	AAC	AAAAG	CC	CAGATAT	TTTAAAT	TGGAGTCTAC	ATGTTCTGAAG	CGCTTGAAT	TGCTGTCT	CTTC	653									
Qy	171	Val	Glu	Asn	Phe	Gln	Arg	Asp	Pro	Thr	Leu	Thr	Trp	Gln	Tyr	Phe	Gly	Ser	Ala	Thr	Gly
Db	654	GTG	GAGAACT	CCAGAG	GAGACCC	AAAGTTG	ACCTGGC	AAATATTTT	TGGCAGTG	CCAACTGGGA	713										
Qy	191	Phe	Phe	Arg	Ile	Tyr	Pro	Gly	Ile	Leu	Trp	Thr	Pro	Asp	Glu	Asn	Gly	Val	Ile	Thr	Phe
Db	714	TTT	CTT	CAGGATCT	ATCCAGG	TATAAAT	TGGACACCTGAT	GAGATG	GAGTGCAT	TACTACT	TTT	773									
Qy	211	Asp	Cys	Arg	Asn	Arg	Gly	Tyr	Trp	Ile	Gln	Ala	Ala	Thr	Ser	Pro	Leu	Ser	Asp	Ile	Val
Db	774	GACT	GCCGAA	CCCGG	TGTGTAT	CAACGCTGCTACT	CTCTCC	CAAGGACATAGT	AGT	833											
Qy	231	Leu	Val	Asp	Val	Ser	Gly	Ser	Met	Leu	Gly	Leu	Arg	Met	Thr	Ile	Ala	Leu	His	Thr	Ile
Db	834	TTG	TGTGAC	GTGAG	CGGAGATATGAAG	GGGTGAGGATGACT	ATG	CCAAAGC	ACCA	CAATC	893										
Qy	251	Thr	Thr	Ile	Leu	Asp	Thr	Leu	Gly	Val	Asn	Asp	Phe	Val	Asn	Ile	Ile	Ala	Tyr	Asn	Asp
Db	894	ACC	ACCATCT	TGGACAC	CCCTGGG	GGAGAA	TGACTTCGTTAAT	ATATCATAG	CGTAC	AAATGAC	953										
Qy	271	Tyr	Val	His	Tyr	Ile	Glu	Pro	Cys	Phe	Leu	Ser	Gly	Ile	Leu	Val	Gln	Ala	Asp	Arg	Asn
Db	954	TAC	TGTCAT	TACAT	CGAGCCTTGTTTAAAG	GGATCTCTCGTCC	AGGCGGGA	CCGAGACAAT	1013												
Qy	291	Arg	Glu	His	Ser	Phe	Leu	Leu	Val	Glu	Glu	Leu	Met	Val	Leu	Ser	Gly	Val	Gly	Val	Val
Db	1014	CGAG	GACATTTCAA	ACTGCTG	TGGAGAGATTGATGGT	CAAGGTG	GGGGTCTG	TGAC	1073												
Qy	311	Gln	Ala	Leu	Arg	Glu	Ala	Phe	Gln	Ile	Leu	Ser	Gln	Phe	Gln	Gln	Ala	Leu	Ser	Gln	Gly
Db	1074	CAAG	CCCTGAGAGA	AGCCTTCCAGAT	CCTGAAG	CAGTTC	CAAGAGG	CCAGCAAG	CAAGGAAGC	1133											
Qy	331	Leu	Cys	Asn	Gln	Ala	Ile	Met	Leu	Ile	Ser	Asp	Gly	Ala	Val	Glu	Asp	Tyr	Glu	Pro	Val
Db	1134	CTCT	GTCAAC	CAGG	CCATCATGCT	CATCAG	CGACGGCGGTGGAGG	ACTAC	AGCCGGTG	1193											
Qy	351	Phe	Glu	Leu	Ser	Asn	Tyr	Pro	Asp	Cys	Leu	Val	Arg	Val	Phe	Thr	Tyr	Leu	Ile	Gly	Arg
Db	1194	TTT	GAGAAG	TATAACT	GCCAGACTGTGAAG	GTCCGAGTTTTC	ACTTACCT	CATTGGGAGA	1253												
Qy	371	Glu	Val	Ser	Phe	Ala	Asp	Arg	Met	Lys	Trp	Ile	Ala	Cys	Asn	Asn	Leu	Ser	Gly	Tyr	Thr
Db	1254	GAAG	TGCTTTTG	TGACCG	CATCGAGT	GGATTG	CATGCCAAC	CAAAAGG	CGTACTAC	ACG	1313										
Qy	391	Gln	Ile	Ser	Thr	Leu	Ala	Asp	Thr	Gln	Glu	Asn	Val	Met	Glu	Tyr	Leu	His	Val	Leu	Ser
Db	1314	CAGAT	CTCAAC	CGCTGG	CGGACAC	CCGAGAGAA	CGTGTG	GAATACCT	TGCACT	GCAC	CAACAAAGG	CGTACTAC	ACG	1373							
Qy	411	Arg	Pro	Met	Val	Ile	Asn	His	Asp	His	Asp	Ile	Trp	Thr	Glu	Ala	Tyr	Met	Asp	Ser	430
Db	1374	CGCCCC	ATGGT	CATCAAC	CCACGAC	GCATCATCTGG	ACAGAGG	CGCTAC	ATGG	ACAGG	CGCTAC	ATGG	ACAGG	CGCTAC	ATGG	ACAGG	CGCTAC	ATGG	ACAGG	CGCTAC	1433
Qy	431	Lys	Leu	Leu	Ser	Ser	Gln	Ala	Gln	Ser	Leu	Thr	Leu	Leu	Thr	Thr	Val	Ala	Met	Pro	Val

Db	1434	AAAGCTCTCAGCTCGCAGGCTCAGAGCCTGACACTCTCTCACCACCTGTGGCCATGCCAGTC	1493
Qy	451	PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp	470
Db	1494	TTCCGCAAGAAGAACCAACCGCATCCCATGGGATTTCTCTGGGTGTGGCTCAGAT	1553
Qy	471	ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr	490
Db	1554	GTGGCCCTCAGAGAGCTGATGAAGCTGGCCCGCCCGGTACAAGCTTGGAGTGCACGGATAC	1613
Qy	491	AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr	510
Db	1614	GCCTTTCTGAACACCAACCAATGGCTACATCTCTCCCATCCCGACCTCCGGCCCTGTAC	1673
Qy	511	ArgGluGlyLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal	530
Db	1674	AGAGAGGGGAAGAACTAAACCCCAACCTAACTACAACAGTGTGATCTCTCCGAAGTG	1733
Qy	531	GluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr	550
Db	1734	GAGTGGGAAGACCAGGCTGNACTCTCTGAGNACAGCCATGATCAATAGGGAACAGGFACT	1793
Qy	551	LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn	570
Db	1794	CTCTCGATGGATGTGAAGGTTCCGATGGATAAAGGAAGCAGAGTTCTTTTCTTGACCAAT	1853
Qy	571	AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg	590
Db	1854	GACTACTCTTTCACGGACATCAGCGACACCCCTTTTCAGTTTGGGGTGTGTCTCCCGG	1913
Qy	591	GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu	610
Db	1914	GGCCACGGAGATACATCTCTTGGGGGAACAGTCTGTGGAGAAGGCCCTGCATGACTTG	1973
Qy	611	LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro	630
Db	1974	CTTACCCAGACCTGGCCCTGGCCGGTGACTGGATCTACTGCATCACAGATATGACCCA	2033
Qy	631	AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro	650
Db	2034	GACCACCGGAAGCTCAGCAGCTAGAGGGCCATGATCCGCTTCTCTACACGGAAGGACCCA	2093
Qy	651	AspLeuGluCysAspGluLeuValArgGluValLeuPheAspAlaValValThrAla	670
Db	2094	GACCTGAGGTGTACGAGGAGCTGGTCCGGAGGTCTGTTTGACCGCGTGTGTGACAGCC	2153
Qy	671	ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisVal	690
Db	2154	CCCATGGAAGCCTACTGGACAGCGCTGGCCCTCAACATGTCCGAGGAGTCTGAACACGTG	2213
Qy	691	ValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerLeuPheValGly	710
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Qy	711	SerGluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThr	730
Db	2274	TCCGAGAAGGTCTCCGACAGGAAGTTCTTGACNACCTGAGGACGAGGCCAGGTGTTCACC	2333
Qy	731	LeuAspArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheVal	750
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Qy	751	PheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAla	770
Db	2394	TTCAACCTCCGCTGGGCAGGAAGACCAAGAGTGGCGGGTGAACCCATGTGTGGTGAACGCA	2453
Qy	771	SerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaGlyVal	790
Db	2454	AGCACAGCTGTGGCGGTGACCGTGGACAGAGACAGCCATTTGCTGCAGCCGCGGGGCTC	2513
Qy	791	GlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThr	810


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Qy TyrAspTyrGlnAlaMetCysLysProSerHisHisSerAlaAlaGlnProLeu 890
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Qy ThrAspProThrCysAspCysSerIlePheProProValLeuGlnGluAlaThrGluVal 1010
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Qy LysTyrAenAlaSerValLysCysAspArgMetArg 1022
Db AAATATAATGCTCTGTCAAATGTGACCGGATGCGC 3209

RESULT 9
AAS17581
ID AAS17581 standard; cDNA; 3228 BP.
AC AAS17581;
XX
XX
XX 26-FEB-2002 (first entry)
DT
XX
XX DNA encoding novel secreted protein #10.
DE
XX
XX Secreted protein; cytostatic; immunosuppressive; vulnery; vaccine;
KW antiinflammatory; neuroprotective; nephrotropic; cardiovascular; human;
KW cancer; autoimmune disease; wound healing disorder; infection;
KW haematopoietic disorder; inflammatory disorder; infertility;
KW neurological disease; psychiatric disease; cardiovascular disease;
KW respiratory disease; renal; gastrointestinal; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..3228
XX /*tag= a
XX /product= "Human secreted protein"
XX
XX WO200179454-A1.
XX
XX 25-OCT-2001.
PD
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PF
XX
XX
PR 11-APR-2001; 2001WO-US011797.
PR 13-APR-2000; 2000US-0196603P.
PR 24-APR-2000; 2000US-0199417P.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;
XX
XX WPI: 2002-061975/08.
DR P-PSDB; AAU09869.
XX
PT New secreted proteins or polypeptides, useful for treating e.g. cancer,
PT autoimmune diseases, wound healing disorder, infections, hematopoietic
PT disorders, inflammatory disorders, infertility, cancer.
XX
PS Claim 2; Page 41-42; 92pp; English.
XX
CC The invention relates to an isolated novel secreted polypeptide (I) and
CC polynucleotide (II). (I) and (II) are useful for treating cancer,
CC autoimmune diseases, wound healing disorder, infections, haematopoietic
CC disorders, inflammatory disorders, infertility, neurological and
CC psychiatric diseases, cardiovascular diseases, respiratory diseases,
CC renal diseases, or gastrointestinal diseases. These may also be used to
CC treat diseases, abnormalities and disorders caused by abnormal
CC expression, production, function and/or metabolism of the genes, as
CC vaccines for inducing immunological response in a mammal, and in
CC screening methods for detecting the effect of added compounds on the
CC production of mRNA and polypeptide in cells. The polypeptides can be used
CC as immunogens to produce antibodies immunospecific for the polypeptides,
CC and to identify membrane-bound or soluble receptors. The polynucleotides
CC may be used as diagnostic reagents, in chromosome localisation studies,
CC and in tissue expression studies. The present sequence represents the
CC coding sequence of novel human secreted protein #10
XX
SQ Sequence 3228 BP; 749 A; 897 C; 932 G; 650 T; 0 U; 0 Other;
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Alignment Scores:

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Pred. No.: 0 Length: 3228
Score: 5234.50 Matches: 1013
Percent Similarity: 95.68% Conservative: 7
Best Local Similarity: 95.03% Mismatches: 34
Query Match: 91.42% Indels: 13
DB: Gaps: 3
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US-09-833-222A-10 (1-1090) x AAS17581 (1-3228)

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Db 58 AGAGTGAAGCTATGGGCTGACACCTTCGGCGGGACCTGTATACACTGTGACCAATAC 117
Qy 32 SerGlySerLeuLeuGlnLysLysValGlyAspValGluSerSerLeuLysTleGlu 51
Db 118 TCAGGCTCTCTCTGTGTCAGAGAAGTACAAAGATGTGGAGTCCAGTCTCAAGATCGAG 177
Qy 52 GluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAenMetLeuArg 71
Db 178 GAGGTGATGGCTTGGAGCTGGTGAGGAAGTTCTCAGAGGACATGGAGAACATCTCTGG 237
Qy 72 ArgLysValGluAlaValGlnAenLeuValGluAlaGluAlaAsePleuAenHis 91
Db 238 AGGAAAGTCGAGGCGGTCCAGAAATCTGGTGAAGTCCCGAGGAGGCGGACCTGAACCC 297
Qy 92 GluPheAenGluSerLeuValPheAspTyrTyrAenSerValLeuIleAenGluArgAsp 111
Db 298 GAATTCAATGAATCCCTGGTGTTCGACTATTACAACTCGGTCTCGATCAACGAGGGAC 357
Qy 112 GluLysGlyAenPheValGluLeuGlyAlaGluPheLeuLeuGluSerAenAlaHisPhe 131
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Qy 172 GluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGlyPhe 191
Db 538 GAGAACTTCCAGAGAGACCCAACTGGTGGCAATATTTGGCAGTGCACATGGGATTC 597
Qy 192 PheArgIleTyrProGlyIleLeuTyrTrpThrProAspGluAsnGlyValIleThrPheAsp 211
Db 598 TTCAGGATCTATCCAGGTATAAAATGGACACTCTGATGAGAATGGAGTCATTACTTTTGAC 657
Qy 212 CysArgAsnArgGlyTyrTrpTyrIleGlnAlaAlaThrSerProLysAspIleValIleLeu 231
Db 658 TGCCGAAACCGCGCTGGTACATTCAAAGCTGCTACTTCTCCCAAGGACATAGTGATTTTG 717
Qy 232 ValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIleThr 251
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Qy 292 GluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAspGln 311
Db 898 GAGCATTTCAAACCTGCTGTGTGAGGAGTTGATGTGTCAAAGTGTGGGGGTCTGTGGACAA 957
Qy 312 AlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySerLeu 331
Db 958 GCCCTGAGAGAGCCTTCCAGATCCTCAAGCAGTTTCCAAAGAGGCCAAGCAAGGAGCCTC 1017
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Db 1018 TGCAACCAAGCCCATCATGCTCATCAGCGACGCGCGCTGTGAGGACTACAGACCGCGTGTTT 1077
Qy 352 GluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrTrpLeuIleGlyArgGlu 371
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Db 1498 TTTCAGACACCAACAATGSGCTACATCCTCTCCCATCCCGACCTCCGCCCTGTACAGA 1557
Qy 512 GluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluValGlu 531
Db 1558 GAGGGGAAGAAATAAAACCAACCTAACTACAACAGTGTGGATCTCTCCGAAGTGGAG 1617
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591 GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu 610
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611 LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630
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2452 AGCACAGCTGTGGCGGTGACCGCTGGACAGAGGACAGCCATTGCTGCAGCCGCGGGCTC 2511
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Qy 171 ValGluAsnPheGlnArgAspProThrLeuThrTrpGlnTyrPheGlySerAlaThrGly 190
Db 654 GTGGAGAACTTCCAGAGAGACCCAAACGTTGACCTGGCAATATTTTGGCAGTGAACCTGGA 713
Qy 191 PheAerGileTyrProGlyIleLeuValTrpThrProAspGluAsnGlyValIleThrPhe 210
Db 714 TTCTTCAGGATCTATCCAGGTATATAATGGACACCTGATGAGAAATGGAGTCATACTTTT 773
Qy 211 AspCyAerGlnArgGlyTrpIleGlnAlaThrSerProIysAspIleValIle 230
Db 774 GACTCGCGAAACCGCGCTGGTACATTCAAAGCTGCTACTTCTCCCAAGGACATAGTGATT 833
Qy 231 LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle 250
Db 834 TTGGTGACGTGAGCGCATATGAAGGGGCTGAGGATGACTATTCGAAGACACCATC 893
Qy 251 ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp 270
Db 894 ACCACCATCTTGGACACCTTGGGGGAGAAATGACTTCRTTAATATCATAGGTACATATGAC 953
Qy 271 TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn 290
Db 954 TAGCTCCATTTACATCGAGCCTTGTTTTAAAGGGATCCTCGTCAGGCGGACCCGAGACAAT 1013
Qy 291 ArgGluHisPheLysLeuLeuValGluGluLeuMetValLysGlyValGlyValValAsp 310
Db 1014 CGAGAGCATTTCAAACTGCTGGTGGAGAGGTGATGTTCAAGGTGTGGGGTGTGGAC 1073
Qy 311 GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer 330
Db 1074 CAAGCCTCGAGAGAAGCCTTCCAGATCCTGAAGCAGTTCCAGAGGCCAAGCAAGGAGC 1133
Qy 331 LeuCyAerGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal 350
Db 1134 CTCTGCAACCCAGGCCATCATGCTCATCAGCGACGGCGCTGAGGACTACGAGCGCGTG 1193
Qy 351 PheGluLysTyrAsnTrpProAspCyValLysValArgValPheThrTyrLeuIleGlyArg 370
Db 1194 TTTGAGAAGTATAACTGGCCAGACTGTAAAGGTCCGAGTTTTCATCTACCTCATTTGGGAGA 1253
Qy 371 GluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThr 390
Db 1254 GAAGTGTCTTTCTGACCGCATGAAGTGGATTGCATGCACCAACAAAGGCTACTACAG 1313
Qy 391 GlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer 410
Db 1314 CAGATCTCAACGCTGGCGGACACCCAGGAGAACGTGATGGAATACCTGCACCGTGTCTCAGC 1373
Qy 411 ArgProMetValIleAsnHisAspHisAspIleIleTrpThrGluAlaTyrMetAspSer 430
Db 1374 CGCCCCATGTTATCAACACGACCCAGCATCATCTGGACAGAGCCCTACATGGACAGC 1433
Qy 431 LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProVal 450
Db 1434 AAGCTCCTCAGCTCGCAGGCTCAGAGCTGACACTGCTCACCACCTGTGGCCATGCCAGTC 1493
Qy 451 PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp 470
Db 1494 TTCAGCAAGAAGAACCAACCGCATCCCATGGCATTTCTCTGGGTGTGGGGCTCAGAT 1553
Qy 471 ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr 490
Db 1554 GTGGCCTCGAGAGAGCTGATGAAGCTTGGCGCCCCCGGTACNAGTTTGGATGGACGGATAC 1613
Qy 491 AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr 510
Db 1614 GCCTTTCTGAACCAACCAATGCTATCTCTCCCATCCCGACCTCCGGGCCCTGTAC 1673
Qy 511 ArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal 530
Db 1674 AGAGAGGGGAAGAAACTAAACCCCAACCTTAACACAGTGTGGATCTCTCCGAAGTG 1733

Qy 531 GluTrpGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
Db 1734 GAGTGGGAAGACCAAGCTGAAATCTCTGAGAACAGCCATGATCAATAGGAAACAGGTACT 1793
Qy 551 LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570
Db 1794 CTCTCGATGGATGTGAAGGTCCGATGGATAAAGGGAAGCGAGTCTCTTTTCTTGACCAAT 1853
Qy 571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
Db 1854 GACTACTTCTTACCGACATCAGCGACACCCCTTTCAGTTTGGGGTGTGCTGTCCCGG 1913
Qy 591 GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu 610
Db 1914 GGCCACGAGAAATACATCTTCTGGGGAAACAGCTCTGTGGAAAGAGCCTGCATGACTTG 1973
Qy 611 LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630
Db 1974 CTTTACCCAGACCTGGCCCTGGCCGTGACTGGATCTACTGCATCACAGATATTGACCCA 2033
Qy 631 AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro 650
Db 2034 GACCACCGGAAAGCTCAGCCAGCTAGAGGCCATGATCCGCTTCTCCACGAAAGGACCCA 2093
Qy 651 AspLeuGluCysAspGluGluLeuValArgGluValLeuPheAspAlaValValThrAla 670
Db 2094 GACCTGGAGTGTGACGAGAGGTGGTCCGGGAGGTGCTGTTTGACCGGGTGTGACAGCC 2153
Qy 671 ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisVal 690
Db 2154 CCCATGGAAAGCCTACTGGACAGCGCTGGCCCTCAACATGTCCGAGGAGTCTGAACAGTG 2213
Qy 691 ValAspMetAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGly 710
Db 2214 GTGGACATGGCCTTCTGGGCACCCCGGCTGGCCTCTGAGAAGCAGCTGTTCGTGGGC 2273
Qy 711 SerGluLysValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThr 730
Db 2274 TCCGAGAAGGTCTCCGACAGGAAGTTCCTGCACACCTGAGGACGAGCCAGCGTTCACC 2333
Qy 731 LeuAspArgPheProLeuTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheVal 750
Db 2334 CTGGACCGCTTCCCGTGTGTACCCGCCAGGCTCAGAGCATCTCTGTCGTCAGCTTCGTC 2393
Qy 751 PheAsnLeuArgTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAla 770
Db 2394 TTCAACCTCCGCTGGCGAGAGACCAGAAAGTGGCGGGTGAACCCATGGTGGTGACGGCA 2453
Qy 771 SerThrAlaValAlaValThrValAspLysArgThrAlaIleAlaAlaAlaGlyVal 790
Db 2454 AGCACAGCTGTGGCGGTGACCGTGGACAGAGAGGACAGCCATTTGCTGCACCGCGGGCGTC 2513
Qy 791 GlnMetLysLeuGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThr 810
Db 2514 CAAATGAAGCTGGAATTTCTCCAGCGCAAAATCTTGGCGGCAACGCGGAGTCAGCACT 2573
Qy 811 ValAspGlyProTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAsp 830
Db 2574 GTGGATGGGCCGTGACACAGAGCTCGAGGACAGTGATCTGGACTGCTTCGTCTATCGAC 2633
Qy 831 AsnAsnGlyPheIleLeuIleSerLysArgSerArgGluThrGlyArgPheLeuGlyGlu 850
Db 2634 AACACGGGTTTCACTCTGATCTCCAGAGGTCCCGAGAGACGGGAAGATTTTCTGGGGAG 2693
Qy 851 ValAspGlyAlaValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMet 870
Db 2694 GTGGATGGTGTGCTCTGACCCAGCTGCTCAGCATGGGGGTGTTACGCAAGTACTATG 2753
Qy 871 TyrAspTyrGlnAlaMetCysLysProSerSerHisHisSerAlaAlaGlnProLeu 890
Db 2754 TATGACTATCAGGCCATGTGCAAAACCTCTGATGCACCAACAGTGCAGGCCAGCCCTG 2813

Qy	891	ValSerProIleSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnLeuValLeu	910
Db	2814		2872
		GTCAAGCCCAATTTCTGCGCTTCTTACGCGCGACCAAGGTGGCTGCTGCAGGAGCTGGTGCT-	
Qy	910	-----	910
Db	2873	TGTGAGTGGGGGTAGACACGGGGCTGGTGGAGGCTGCATGCGAGGGTGGCTTAGGAGGGT	2932
Qy	910	-----	910
Db	2933	GTCTTGTATCAGGAGGCTGCAAGGTCTCAGGACAAACCACTTGTCTACCAAGACCCCGGG	2992
Qy	910	-----	910
Db	2993	GAAGGAGGGCAAAATCCCTGGGCATGAGCGCCACTCTTCTCTGCATGCTTTGGCCCTGGG	3052
Qy	910	-----	910
Db	3053	AGGGACCTCATTTGCTCAACCAGAGCCCTCAAGCAGGGNAGAGGCTGTCTCTGGAGGAGG	3112
Qy	910	-----	910
Db	3113	GGATGGCCGGGGCTGTTCAGGGATACTCCAGCTCTCTGGGAACCCAAAGTCGGGAGGGCT	3172
Qy	911	-----PheLeuLeuGluTrpSerValTrp	918
Db	3173		3232
		CAGAGGCTCCGAGATTCAAGTCTGTGTCTGACAGGTTCTCTGTCTGGAGTGGAGTGTCTGG	
Qy	919	GlySerTrpTrpAspArgGlyValaglu-----	927
Db	3233		3292
		GGCTCTGGTACGACAGAGGGGCCGAGGGTGAGTGCAAGAGCTGCAGGGCCATGTCTGT	
Qy	927	-----	927
Db	3293	AAGAGCAGTGGCATTTTGGTCCACTAAGCTGAGACCACTCCCTGTGGGTGGGTGACAGT	3352
Qy	927	-----	927
Db	3353	GGGGATAGGTGACCCCTGAAGCATCGTTTTCACATCTCACCTTCGCTGGCCTTCTCTCAT	3412
Qy	927	-----	927
Db	3413	CACATCCTCACTCCTGGCTGTGTGTGACATCATCTTGGGACACCGCCACATCCATGTG	3472
Qy	927	-----	927
Db	3473	CCATCATCACCAACCCCATGACATCTGCCCTCATGTGCCACCATGTTTTCTGTGCGGTG	3532
Qy	928	-----AlaLysSerValPheHisHisSerHisLys	937
Db	3533		3592
		TCCACCTGTGCTGGGCTTATGTTCCGGCCAGCCAAAGTGTCTTCCATCACATCCCAAA	
Qy	937	sHisLysLysGlnAspProLeuGlnProCysAspThrGluTrpProValPheValTrpGln	957
Db	3593		3652
		ACAAAGAAGCAGACACCGCTGTCAGCCCTCGCACACGGAGTACCCCGTGTTCGTGTACCA	
Qy	957	nPro-AlaIleArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLysValPheVal	977
Db	3653		3712
		CGCGGNCATCCGGAGGCCNACGGGATCGTGGAGTGGCGGCCCTCGCAGAGAGGTATTG	
Qy	977	alValGlnGlnIleProAsnSerAsnLeuLeuLeuValThrAspProThrCysAspC	997
Db	3713		3772
		TGGTGCAGCAGATTCCCAACAGTAACCTCTCTCTCTGGTGACAGACCCACCTGTGACT	
Qy	997	ysSerIlePheProProValLeuGlnGluAlaThrGluValLysTrpAsnAlaSerValL	1017
Db	3773		3832
		GCAGCATCTTCCCAACCAAGTCTCGAGAGGCGCAGAAAGTCAAATATAATGCCTCTGTGCA	
Qy	1017	ysCysAspArgMetArgSerGlnLysLeuArgArgProAspSerCysHisAlaPheH	1037
Db	3833		3892
		AATGTACCGGATGCGCTCCAGNAGCTCCGCGCGGACACAGACTCTCTGCACGCGCTTCC	
Qy	1037	isProGluValArgValGluAlaAspArgGlyTrpAlaGlyPheSerSerProAsnProL	1057

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Db      3893 ATCCAGAGGAGAATGCCAGACTGGCGGYGCCTCGGACACCTCAGCTCGCCGCC 3952
Qy      1057 euCyseLeuGliYLeuCysProCyArGlnclnluHisIleGliYMetProMetAasnThrPro 1076
Db      3953 TACTCTGTCT-GCCTGTGTGTGCTGGGGGCTACTGCCCCAACTCTCTGCGGTGACACCA 4010

RESULT 12
AAS01431
ID ID AAS01431 standard; cDNA; 3201 BP.
XX AC AAS01431;
XX
DT 04-JUL-2001 (first entry)
XX
DE Human secreted soluble alpha2delta calcium channel subunit #16 cDNA.
XX
KW Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;
KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;
KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;
KW filter binding assay; wheat germ lectin flashplate assay; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 3..3201
FT FT /*tag= a
FT FT /partial
FT FT /product= "Alpha2delta calcium channel subunit #16"
FT FT /note= "this sequence lacks a stop codon"
FT FT /transl_except= {pos:2286..2340,aa:Ser-Asp}
FT FT /note= "These two codons between them have an apparent 49
FT FT nucleotide insertion which alters the reading frame"
PN WO200119870-A2.
XX
PD 22-MAR-2001.
XX
PF 18-SEP-2000; 2000WO-EPO09137.
XX
PR 16-SEP-1999; 99US-00397550.
XX
PA (WARN ) WARNER LAMBERT CO.
XX
PI Brown JP, Bertelli F;
DR WPL; 2001-235262/24.
DR P-PSDB; AAU01036.
XX
XX Calcium channel alpha2delta subunits, useful in e.g. SPA assays,
PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or
PT Wheat Germ Lectin Flashplate assays.
XX
PS Claim 39; Page 146-147; 160pp; English.
XX
XX The present sequence encodes for human secreted calcium channel
CC alpha2delta subunit #16 which is soluble and retains the functional
CC characteristics of the full length or wild type alpha2delta subunit
CC (AAU01035) from which it is derived. The invention relates to truncated
CC alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins
CC which retain their affinity for radioactively labelled gabapentin. The
CC alpha2delta subunit is 1 of the components of the heteromultimeric
CC voltage-dependent calcium channel (VDCC) complexes present in neuronal
CC and non-neuronal tissues including heart and skeletal muscle. Numerous
CC soluble forms of the human calcium channel alpha2delta subunits (AAU01014
CC -AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the porcine
CC calcium channel alpha2delta subunits (AAU01027-AAU01031) are described.
CC The secreted soluble alpha2delta subunit may be used in assays e.g.
CC scintillation proximity assay (SPA), flashplate, nickel flashplate,
CC filter binding or wheat germ lectin flashplate assays to detect or
CC measure the binding or interaction of a ligand (e.g. gabapentin, L-
CC Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine, L-
CC Valine, Spermine and/or L-Phenylalanine) of a calcium channel alpha2delta

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Qy 671 ProMetGluAlaTyrTrpThrAlaLeuAlaLeuMetSerGluGluSerGluHisVal 690
Db 2154 CCCATGGAAGCCTACTGACAGCGCTGGCCCTCAACATGTCGAGGAGTCTGAACAGTG 2213
Qy 691 ValAspMetAlaPheLeuGlyThrArgAla----- 700
Db 2214 GTGGACATGGCCTTCTGGGACACCGGGCTGGCCCTCTGAGAAGCAGCTGTTCGTGGGC 2273
Qy 701 -----GlyLeuLeuArgSerSerLeuPheValGlySerGluLysVa 714
Db 2274 TCCGAGAAGGTCTCCGAGTGGCCTCTCTGAGAAGCAGCTTGTTCGTGGCTCCGAGAAGGT 2333
Qy 714 iSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeuAspArgPh 734
Db 2334 CTCCGACAGAAGTTCCTGACACCTGAGGACGAGGCCAGCGTGTTCACCTGGACCGCTT 2393
Qy 734 eProLeuTyrTrpArgGlnAlaSerGluHisProAlaGlySerPheValPheAsnLeuAr 754
Db 2394 CCGCTGTGTACCGCCAGCGCTCAGAGCATCTCTGCTGGCAGCTTCTCTTCAACCTCCG 2453
Qy 754 gTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAlaSerThrAlaVa 774
Db 2454 CTGGCAGAGAAGGACCAAGAGTGGGGTGAACCCATGCTGGTGGTGGTGGTGGTGGTGGT 2513
Qy 774 lAlaValThrValAspLysArgThrAlaAlaAlaAlaAlaGlyValGlnMetLysLe 794
Db 2514 GCGGTGACCGTGGACAAAGAGGACAGCCATTTGCTGACGCGCGCGCGCTCCAAATGAAGCT 2573
Qy 794 uGluPheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThrValAspGlyPr 814
Db 2574 GGAATTCCTCAGCGCAAAATTCCTGGCGGCAACCGCGCAGTGGCAGCACTGTGGATGGCC 2633
Qy 814 oTyrThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAspAsnAsnGlyPh 834
Db 2634 GTGCACACAGAGCTGCGAGGACAGTGATCTGGACTGCTTCTGTCATCGACACAACGGTT 2693
Qy 834 eLleLeuLysSerLysArgSerArgGluThrGlyArgPheLeuGlyGluValAspGlyAl 854
Db 2694 CATTCGATCTCCAAAGAGTCCCGAGAGCGGGAAGATTCTCGGGGAGGTGGATGGTC 2753
Qy 854 aValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMetTyrAspTyrGl 874
Db 2754 TGTCTGACCCAGCTGCTCAGCATGGGGGTGTTCCAGCAAGTGACTATGATGACTATCA 2813
Qy 874 nAlaMetCysLysProSerSerHisHisSerAlaAlaGlnProLeuValSerProIl 894
Db 2814 GGCCATGTGCAAAACCTCGAGTCACCAACACAGTGCAGCCAGCCCTGCTGAGCCCAAT 2873
Qy 894 eSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluValLeuPheLeuGlu 914
Db 2874 TTCTGCCCTTCTGACGCGCAGCAGGTGGCTGCTGCAGGAGCTGTGTCTCTGCTGGA 2933
Qy 914 uTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSerValPheHisHi 934
Db 2934 GTGGAGTGTCTGGGGCTCTCTGGTACGACAGGGGCGGAGCCCAAAAGTGTCTTCATCA 2993
Qy 934 sSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrProValPh 954
Db 2994 CTCCCAAAACACAAAGAAGCAGGACCCGCTGCAGCCCTGCGACACGAGTACCCCGTGT 3053
Qy 954 eValTyrGlnProAlaIleArgGluAlaAsnGlyIleValGluCysGlyProCysGlnLy 974
Db 3054 CGTGTACAGCCGCGCATCCGGGAGGCCAACGGGATCGTGGAGTGGCGGCGCTGCCAGAA 3113
Qy 974 eValPheValValGlnGlnIleProAsnSerAsnLeuLeuLeuValThrAspProTh 994
Db 3114 GGTATTTGTGGTGAGCAGATTTCCAACAGTAACTCTCTCTCTGTTGACAGACCCAC 3173
Qy 994 rCysAspCysSerIlePheProProVal 1003
Db 3174 CTGTGAGTCGAGCATCTTCCACACAGTG 3201
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RESULT 13

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AAF57568
ID AAF57568 standard; DNA; 3201 BP.
XX
AC AAF57568;
XX
DT 11-JUN-2001 (first entry)
XX
DE Human calcium channel alpha2delta subunit encoding DNA.
XX
KW Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;
KW nervous system disorder; pain; epilepsy; anxiety; human; ds.
XX
OS Homo sapiens.
XX
PN WO200120336-A2.
XX
PD 22-MAR-2001.
XX
PF 18-SEP-2000; 2000WO-EP009136.
XX
PR 16-SEP-1999; 99US-00397549.
XX
PA (WARN ) WARNER LAMBERT CO.
XX
PI Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;
DR WPI; 2001-257902/26.
XX
PT Competitive binding assay for screening ligands which bind a cerebral
PT cortical voltage-dependent calcium channel alpha2-delta-1 subunit, where
PT the ligands identified are useful for treating disorders of the nervous
PT system, including pain.
XX
PS Disclosure; Page 144-145; 158pp; English.
XX
CC The invention relates to a new method for screening ligands which bind a
CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,
CC preferably alpha2delta-1 subunit. The method comprises contacting a
CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of
CC interest and a labelled compound which binds the subunit, followed by
CC measuring the level of binding of the labelled compound to alpha2delta-1
CC subunit. The method is useful for screening ligands, preferably
CC biologically active products that modulate a nervous system function,
CC which bind a cerebral cortical voltage-dependent calcium channel
CC alpha2delta-1 subunit. The ligands identified by the method are useful
CC for treating disorders of the nervous system, including pain, epilepsy
CC and anxiety. The present sequence represents a human calcium channel
CC alpha2delta subunit encoding DNA
XX
SQ Sequence 3201 BP; 748 A; 888 C; 921 G; 644 T; 0 U; 0 Other;
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Alignment Scores:
Pred. No.: 0 Length: 3201
Score: 5148.00 Matches: 989
Percent Similarity: 98.02% Conservative: 1
Best Local Similarity: 97.92% Mismatches: 3
Query Match: 89.91% Indels: 17
DB: 5 Gaps: 1
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US-09-833-222A-10 (1-1090) x AAF57568 (1-3201)

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Qy 11 AspArgValLysLeuTrpAlaAspThrPheGlyAspLeuTyrAsnThrValThrLys 30
:::
Db 174 GAAACAGTGAAGCTATGGCTGACACCTTCGGCGGGAGCTGTATTAACACTGTGACCAA 233
Qy 31 TyrSerGlySerLeuLeuGlnLysLysTyrLysAspValGluSerSerLeuLysIle 50
Db 234 TACTCAGGCTCTCTTCTGTCTGCAGAAAGTCAAGGATGGAGTCCAGTCTCTGAAGATC 293
Qy 51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
Db 294 GAGGAGTGGATGGCTTGGAGCTGGTGGAGGAGTTCTCAGAGGACATGGAGACATGCTG 353
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Qy 71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn 90
Db 354 CGGAGGAAAGTCGAGGCGGTCAGAAATCTGGTGAAGCTGCCGAGGAGCGGACCTGAAC 413
Qy 91 HisGluPheAsnGlnSerLeuValPheAspTyrTyrAsnSerValLeuIleAsnGluArg 110
Db 414 CACGAATTCGAATGAATCCCTGGTGTTCGACTATTACAACTCGGTCTCTGATCAACGAGAG 473
Qy 111 AspGluLysGlyAsnPheValGluLeuGlyAlaGluPheLeuLeuGluSerAsnAlaHis 130
Db 474 GACGAGAAGGCAACTTCGTGGAGCTGGGCGCGAGTTCCTCTGGAGTCCAATGCTCAC 533
Qy 131 PheSerAsnLeuProValAsnThrSerIleSerValGlnLeuProThrAsnValTyr 150
Db 534 TTCAGCAACCTGCCGGTGAACACCTCCATCAGCAGCGTGCAGTGCACCACCACTGTAC 593
Qy 151 AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe 170
Db 594 AACAAAGACCAGATATTTTAAATGGAGTCTACATGTCTGAAGCCTTGAATGCTGTCTTC 653
Qy 171 ValGluAsnPheGlnArgAspProThrLeuThrTropGlnTyrPheGlySerAlaThrGly 190
Db 654 GTGGAGAACTTCAGAGAGACCAACGTTGACCTGGCAATATTTTGGCAGTGAACCTGGA 713
Qy 191 PhePheArgIleTyrProGlyIleLysTyrThrProAspGluAsnGlyValIleThrPhe 210
Db 714 TTCTTCAGGATCTATCCAGGTATAAATGACACCTGATCAGAAATGGAGTCAATACTTTT 773
Qy 211 AspCysArgAsnArgGlyTyrTyrIleGlnAlaThrSerProLysAspIleValIle 230
Db 774 GACTCGCGAAACCGCGCTGGTACATTCAAAGCTGCTACTTCTCCCAAGGACATAGTGATT 833
Qy 231 LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle 250
Db 834 TTGGTGACGTGAGCGGCAGTATGAAGGGGCTGAGGATGACTATGTCCAAAGCACACCATC 893
Qy 251 ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp 270
Db 894 ACCACCATCTTGGACACCTTGGGGGAGAAATGACTTCGTGTTAATATCATAGGCTACAATGAC 953
Qy 271 TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn 290
Db 954 TAGCTCCATTACATCGAGCCTTGTTTTAAAGGATCCTCGTCAGGCGGACCGAGACAAT 1013
Qy 291 ArgGluHisPheLysLeuLeuValGluLeuMetValLysGlyValGlyValValAsp 310
Db 1014 CGAGAGCATTTTCAAACGTCTGGTGGAGAGTTGATGTCAAAGGTGTGGGGGTCTGGGAC 1073
Qy 311 GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer 330
Db 1074 CAAGCCTTGAGAGAGCCTTCAGATCTCTGAAGCAGTTCCAAAGGGCCCAAGCAAGAGAC 1133
Qy 331 LeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal 350
Db 1134 CTCTGCAACACGAGCCATCATGTCTCATCAGCGCGGCGCTGAGGACCTACGAGCCGGTG 1193
Qy 351 PheGluLysTyrAsnTyrProAspCysLysValArgValPheThrTyrLeuIleGlyArg 370
Db 1194 TTTGAGAAGTATAACTGTGGCCAGACTGTAAAGTCCGAGTTTTCCTTACCTCATTTGGGAGA 1253
Qy 371 GluValSerPheAlaAspArgMetLysTyrIleAlaCysAsnAsnLysGlyTyrTyrThr 390
Db 1254 GAAGTGTCTTTGCTGACCGCATGAAGTGGATTGCAATGCAACCAACAAAGGCTACTACAG 1313
Qy 391 GlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrLeuHisValLeuSer 410
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Qy 411 ArgProMetValIleAsnHisAspHisAspIleTyrThrGluAlaTyrMetAspSer 430
Db 1374 CGCCCCATGTGTATCAACACGACCAACGACATCATCTGGACAGAGGCTTACATGGACAGC 1433
Qy 431 LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrValAlaMetProVal 450

Db 1434 AAGCTCTCTCAGCTCGCAGGCTCAGAGCCTGACACTGCTCACCACCTGTGGCCATGCCAGTC 1493
Qy 451 PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp 470
Db 1494 TTCAGCAAGAAGAACGAAACGCGATCCCATGGCATTTCTCTGGGTGTGGGTCTCAGAT 1553
Qy 471 ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLysLeuGlyValHisGlyTyr 490
Db 1554 GTGGCCTTGAGAGAGCTGATGAAGCTGGCGCCCCGGTACAAAGCTTGGAGTGCACGGATAC 1613
Qy 491 AlaPheLeuAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyr 510
Db 1614 GCCTTTCTGAACACCAACAATGSGCTACATCTCTCCCATCCCGACCTCCGCGCCCTGTAC 1673
Qy 511 ArgGluGlyLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluVal 530
Db 1674 AGAGAGGGGAAGAACTAAACCCAAACCTAATCAACAGTGTGGATCTCTCCGAAGTG 1733
Qy 531 GluTyrGluAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThr 550
Db 1734 GAGTGGGAAGACCAAGCTGAATCTCTGAGAACAGCCATGATCAATAGGGAACAGGTACT 1793
Qy 551 LeuSerMetAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsn 570
Db 1794 CTCTCGATGGATGTGAAGGTTCGATGGATAAAGGGAAGGAGTCTCTTTCTTGACCAAT 1853
Qy 571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
Db 1854 GACTACTTCTTCCGAGACATCAGCAGACACCCCTTTCAGTTTGGGGGTGGTGTCTCCCG 1913
Qy 591 GlyHisGlyGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeu 610
Db 1914 GGCCACGGAGAATACATCTCTTGGGGAACACGTCTGTGGAGAAGAGCCCTGCATGACTTG 1973
Qy 611 LeuHisProAspLeuAlaLeuAlaGlyAspTyrIleTyrCysIleThrAspIleAspPro 630
Db 1974 CTTTACCCACAGCCTGGCCCTTGCGCGTGACTGATCTACTGCATCACAGATATTGACCCA 2033
Qy 631 AspHisArgLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspPro 650
Db 2034 GACCACCGGAAGCTCAGCAGCAGCTAGAGGCCATGATCCGCTTCTCACCAGGAAGGCCCA 2093
Qy 651 AspLeuGluCysAspGluLeuValArgGluValLeuPheAspAlaValValThrAla 670
Db 2094 GACCTGGAGTGTGACGAGAGGCTGTGTCGGGAGGTGCTGTTGACCGGTGTGCACAGCC 2153
Qy 671 ProMetGluAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisVal 690
Db 2154 CCCATGGAAAGCTACTGGACAGCGCTGGCCCTCAACATGTCCGAGGAGTCTGAACAGTG 2213
Qy 691 ValAspMetAlaPheLeuGlyThrArgAla----- 700
Db 2214 GTGGACATGGCCTTCTTGGGCACCCCGGCTGGCCTCTCAGAGAAGCAGCTTGTTCGTGGGC 2273
Qy 701 -----GlyLeuLeuArgSerSerLeuPheValGlySerGluLysVa 714
Db 2274 TCCGAGAAGTCTCCGAGTGGCTCTCTGAGAGCAGCTTGTTCGTGGGTCTCCGAGAGGT 2333
Qy 714 lSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeuAspArgPh 734
Db 2334 CTCCGACAGGAAGTCTCTGACACCTGAGGACGAGGCCAGCGTGTTCACCTTGACCGCTT 2393
Qy 734 eProLeuTyrTrpTyrArgGlnAlaSerGluHisProAlaGlySerPheValPheAsnLeuAr 754
Db 2394 CCCGCTGTGGTACCCCGAGGCTCAGAGCATCTCTGTCGAGCTTCGTCTTCAACCTCCG 2453
Qy 754 gTrpAlaGluGlyProGluSerAlaGlyGluProMetValValThrAlaSerThrAlaVa 774
Db 2454 CTGGGCGAGAGACCAAGAAAGTCCGGGTGAACCCATGGTGGTGACGGCAAGCACAGCTGT 2513
Qy 774 lAlaValThrValAspLysArgThrAlaIleAlaAlaGlyValGlnMetLysLe 794

Db 2514 GCGGGTGAACCTGGACAGAGACAGCATTGCTGCAGCCGCGCTCCAAATGAAGCT 2573

Qy 794 uGlupheLeuGlnArgLysPheTrpAlaAlaThrArgGlnCysSerThrValAspGlyPr 814

Db 2574 GGAATTCCTCAGCGCAAAATTCGGGGCGCAACCGCGCAGTGCAGCACTGTGGATGGGCC 2633

Qy 814 oTyThrGlnSerCysGluAspSerAspLeuAspCysPheValIleAspAenAenGlyPh 834

Db 2634 GTGCACACAGAGCTGCGGAGACAGTGTCTGGACTGTCTGCATCGACACACACAGCGGTT 2693

Qy 834 eIleLeuLeuSerLysArgSerArgGluThrGlyArgPheLeuGlyGluValAspGlyAl 854

Db 2694 CATTCGTATCTCCAAAGAGTCCCGAGAGACGGGAAGATTTCTGGGGGAGGTGGATGGTC 2753

Qy 854 aValLeuThrGlnLeuLeuSerMetGlyValPheSerGlnValThrMetTyrAspTyrGl 874

Db 2754 TGTCTCGACCCAGCTGCTCAGCATGGGGTGTTCAGCCAAAGTACTATGATGACTATCA 2813

Qy 874 nAlaMetCysLysProSerSerHisHisSerAlaAlaGlnProLeuValSerProIl 894

Db 2814 GGCCATGTGCAAAACCTCGAGTCAACCAACAGTGCAGCCAGCCCTGGTGCAGCCCAAT 2873

Qy 894 eSerAlaPheLeuThrAlaThrArgTrpLeuLeuGlnGluLeuValLeuPheLeuLeuGl 914

Db 2874 TTCTGCTCTTGTGACGGCGACAGTGCTGCTGCAGAGCTGGTGTCTCTCTGCTGGA 2933

Qy 914 uTrpSerValTrpGlySerTrpTyrAspArgGlyAlaGluAlaLysSerValPheHisH 934

Db 2934 GTGGAGTGTCTGGGGCTCTGGTACGACAGAGGGCGGCGGCAAAAGTGTCTTCCATCA 2993

Qy 934 sSerHisLysHisLysLysGlnAspProLeuGlnProCysAspThrGluTyrProValPh 954

Db 2994 CTCCCAAAACACAAAGACAGGACCGCGCTGCAGCCCTGCGACACGAGTACCCCGTGT 3053

Qy 954 eValTyrGlnProAlaIleArgGluAlaAenGlyLleValGluCysGlyProCysGlnLy 974

Db 3054 CGTGTACCGCGGCCCATCGGGAGGCCAACGGGATCGTGAGTGGCGGCCCTGCCAGAA 3113

Qy 974 sValPheValValGlnGlnIleProAenSerAsnLeuLeuLeuValThrAspProTh 994

Db 3114 GGATTTGTGGTGACGAGATTCCCAACAGTAACTCTCTCTCTGTGTGACAGACCCAC 3173

Qy 994 rCysAspCysSerIlePheProVal 1003

Db 3174 CTGTGACTGCAGCATCTCCACCAAGTG 3201

RESULT 14

ID ADN33188 standard; DNA; 3742 BP.

AC ADN33188;

XX

XX 18-NOV-2004 (first entry)

XX Human transporter and ion channel (TRICH) gene SeqID73.

XX transporters and ion channel; TRICH; neuroprotective; relaxant;

KW antihypoid; antidiabetic; cytostatic; dermatological; immunosuppressive;

KW antiinflammatory; thymimetic; antiallergic; cerebroprotective;

KW gastrointestinal; hepatotropic; nephrotropic; anticonvulsant;

KW antiparkinsonian; antibacterial; antiparasitic; fungicide; protozoicide;

KW virucide; utropathic; antirheumatic; cardiant; cardiovascular; anti-HIV;

KW neotropic; TRICH agonist; TRICH antagonist; gene therapy;

KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;

KW muscular disorder; myotonic dystrophy; catatonia; endocrine disorder;

KW diabetes; Grave's disease; cancer; leukaemia; cervical cancer;

KW breast cancer; immunological disorder; scleroderma;

KW systemic lupus erythematosus; allergy; gastrointestinal disorder;

KW Crohn's disease; renal disorder; Goodpasture's syndrome; infection;

KW viral; bacterial; fungal; parasitic; protozoal; helminthic;

KW cardiovascular disorder; atherosclerosis; hepatic disease; cirrhosis;

KW transgenic animal; gene; ds; human.

OS Homo sapiens.

XX WO2004035755-A2.

XX

XX 29-APR-2004.

XX

XX 16-OCT-2003; 2003WO-US033087.

XX

XX 16-OCT-2002; 2002US-0419313P.

PR 23-OCT-2002; 2002US-0421033P.

PR 25-OCT-2002; 2002US-0421349P.

PR 04-NOV-2002; 2002US-0423516P.

XX (INCY-) INCYTE CORP.

XX Hafalia AJA, Khare R, Lal PG, Yue H, Baughn MR, Thornton MB;

XX Lu DAM, Ison CH, Becha SD, Ding L, Warren BA, Lee SY, Swarnakar A;

PI Elliott VS, Richardson TW, Marquis JP, Ramkumar J, Murage J;

PI Raumann BE, Yao MG, Lu Y, Gietzen KO, Yang YG, Chang H, Chawla NK;

PI Tran UK, Lee S, Yang J, Gandhi AR, Tribouley CM, Policky JL;

PI Ring HZ, Lee EA;

XX WPI: 2004-348448/32.

DR P-PSDB; ADN33132.

XX

PT New TRICH polypeptides, useful for diagnosing, preventing, and treating

PT disorders associated with abnormal expression or activity of TRICH, e.g.

PT neuromuscular, immunological, cardiovascular disorders, cancer and/or

PT infections.

XX

XX Claim 5; SEQ ID NO 73; 285pp; English.

XX

CC This invention relates to novel human transporters and ion channel

CC (TRICH) proteins and the nucleotide sequences which encode them. The

CC invention may be useful for the production of compounds with a

CC neuroprotective, relaxant, antihypoid, antidiabetic, cytostatic,

CC dermatological, immunosuppressive, antinflammatory, thymimetic,

CC antiallergic, cerebroprotective, gastrointestinal, hepatotropic,

CC nephrotropic, anticonvulsant, antiparkinsonian, antibacterial,

CC antiparasitic, fungicide, protozoicide, virucide, utropathic,

CC antirheumatic, cardiant, cardiovascular, anti-HIV or nootropic activity

CC acting as TRICH agonists or antagonists. In addition the disclosed

CC sequences may be useful for gene therapy. The invention may be useful in

CC diagnosing, preventing, and treating disorders associated with an

CC abnormal expression or activity of TRICH, such as neurodegenerative

CC disorders (for example Parkinson's disease, Alzheimer's disease),

CC muscular disorders (for example myotonic dystrophy, catatonia), endocrine

CC disorders (for example diabetes, Grave's disease), cancers (for example

CC leukaemia, cervical or breast cancers), immunological disorders (for

CC example scleroderma, systemic lupus erythematosus, allergies),

CC gastrointestinal disorders (for example Crohn's disease), renal disorders

CC (for example Goodpasture's syndrome), infections (for example viral,

CC bacterial, fungal, parasitic, protozoal, helminthic), cardiovascular

CC disorders (for example atherosclerosis), or hepatic diseases (for example

CC cirrhosis). TRICH or its fragments may also be used in screening for

CC compounds that specifically bind to and modulate the activity of TRICH.

CC The nucleotides can be used to create humanised animals or transgenic

CC animals to model human disease. The present sequence is that of a human

CC transporter and ion channel (TRICH) gene of the invention.

XX

SQ Sequence 3742 BP; 882 A; 1052 C; 1053 G; 755 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 3742

Score: 5127.50 Matches: 998

Percent Similarity: 92.62% Conservative: 6

Best Local Similarity: 92.07% Mismatches: 31

Query Match: 89.55% Indels: 51

DB: 13 Gaps: 2

US-09-833-222A-10 (1-1090) x ADN33188 (1-3742)

Qy 11 AspArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAenThrValThrLys 30

Db 106 GAAACAGTGAAGCTATGGCTGACACCTTCGGCGGGACCTGTATACACTGTGACCAA 165
Qy 31 TySersGlySerLeuLeuLeuGlnLysGlyTyrLysAspValGluSerSerLeuLysLe 50
Db 166 TACTCAGGCTCTCTCTGCTGCGAAGAAGTACAAAGATGTGGAGTCCAGTCTGAAGATC 225
Qy 51 GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu 70
Db 226 GAGGAGTGTGATGGCTTGGAGCTGGTGAGAGTTCTCAGAGGACATGGAGAACATGCTG 285
Qy 71 ArgArgLysValGluAlaValGlnAsnLeuValGluAlaGluGluAlaAspLeuAsn 90
Db 286 CGAGAGAAAGTCGAGGCGGTCCAGAACTCTGTTGAAGCTGCCGAGGAGCGGACCTGAAC 345
Qy 91 HisGluPheAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuLysLeuArg 110
Db 346 CAGGAATTCGAATCCCTGGGTGTCGACTATTTACAACTCGGTCTGTGATCAACGAGAG 405
Qy 111 AspGluLysGlyAsnPheValGluLeuGlyValaGluPheLeuLeuGluSerAsnAlaHis 130
Db 406 GACGAGAAAGGCAACTTCGTGGAGCTGGGCGCGAGTTCTCTGGAGTCCAAATGCTCAC 465
Qy 131 PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr 150
Db 466 TTCAGCAACCTGCGCGGTGAACACCTCCATCAGCAGCGTGCAGCTGCCCAACAGGTGAC 525
Qy 151 AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaValPhe 170
Db 526 AACAAAGACCCAGATATTTTAAATGGAGTCTACATGTCCTGAAGCCTTGAATGCTCTTC 585
Qy 171 ValGluAsnPheGlnArgAspProThrLeuThrTyrPheGlySerAlaThrGly 190
Db 586 GTGGAGAACTTCAGAGAGACCCACGTTGACCTGGCNAATATTTTGGCAGTGCACCTGGA 645
Qy 191 PhePheArgIleTyrProGlyIleLysTyrThrProAspGluAsnGlyValIleThrPhe 210
Db 646 TTCTTCAGGATCTATCCAGGTATAAAATGGACACCTGATGAGAATGGAGTCATTACTTTT 705
Qy 211 AspCysArgAsnArgGlyTyrPyrIleGlnAlaAlaThrSerProLysAspIleValIle 230
Db 706 GACTGCGGAAACCGCGCTGTATCAATCAAGCTGTACTTCTCCCAAGGACATAGTGATT 765
Qy 231 LeuValAspValSerGlySerMetLysGlyLeuArgMetThrIleAlaLysHisThrIle 250
Db 766 TTGGTGGACGTGAGCGGCAGTATGAAGGGCTGAGGATGACTATTGCCAAGCACACCAATC 825
Qy 251 ThrThrIleLeuAspThrLeuGlyGluAsnAspPheValAsnIleIleAlaTyrAsnAsp 270
Db 826 ACCACCATCTTGGACACCCCTGGGGGAGAAATGACTTCGTTAAATATCATAGCGTACAATGAC 885
Qy 271 TyrValHisTyrIleGluProCysPheLysGlyIleLeuValGlnAlaAspArgAspAsn 290
Db 886 TAGCTCCATTACATCGAGCCTTGTTTAAAGGATCCTCGTCAGCGGACCGAGACAAT 945
Qy 291 ArgGluHisPheLysLeuLeuValGluLeuMetValLysGlyValGlyValValAsp 310
Db 946 CGAGAGCATTTCAAACCTGCTGTGGAGAGTTGATGGTCAAAGGTGTGGGGTCTGGGAC 1005
Qy 311 GlnAlaLeuArgGluAlaPheGlnIleLeuLysGlnPheGlnGluAlaLysGlnGlySer 330
Db 1006 CAAGCCCTGAGAGAAGCCTTCCAGATCTCTGAAGCAGTTCCAGAGGCCAAGCAAGGAAGC 1065
Qy 331 LeuCysAsnGlnAlaIleMetLeuIleSerAspGlyAlaValGluAspTyrGluProVal 350
Db 1066 CTCTGAACACGCGCCATCATGCTCATCAGCAGCGGCGCGTGAGGACTACGAGCCGGTG 1125
Qy 351 PheGluLysTyrAsnTrpProAspCysLysValArgValPheThrTyrLeuIleGlyArg 370
Db 1126 TTTGAGAAGTATAACTGGCCAGACTGTAAAGTCCGAGTTTCACTTACCTCATTTGGGAGA 1185
Qy 371 GluValSerPheAlaAspArgMetLysTrpIleAlaCysAsnAsnLysGlyTyrTyrThr 390

Db 1186 GAAGTGTCTTTTGGCTGACCGCATGAAGTGGATTGCATGCAACAACAAGGCTACTACACG 1245
Qy 391 GlnIleSerThrLeuAlaAspThrGlnGluAsnValMetGluTyrIleuHisValLeuSer 410
Db 1246 CAGATCTCAACGCTGGCGGACACCCAGAGAAAGTGTGTAATACCTGCACGTGCTCAGC 1305
Qy 411 ArgProMetValIleAsnHisAspHisAspIleIleTyrThrGluAlaTyrMetAspSer 430
Db 1306 CGCCCATCTGTCATCAACCGACGACGACATCATCTGGACAGAGCCCTCATCATGGACAGC 1365
Qy 431 LysLeuLeuSerSerGlnAlaGlnSerLeuThrLeuLeuThrThrValAlaMetProVal 450
Db 1366 AAGCTCTCAGCTCGCAGGCTCAGAGCCTGACACTGTTCACCACTGTGGCATGCCAGTC 1425
Qy 451 PheSerLysLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp 470
Db 1426 TTCAGCAAGAAGAACGAAACGCGATCCCATGGCATTTCTCTGGGTGTGGGTCTCAGAT 1485
Qy 471 ValAlaLeuArgGluLeuMetLysLeuAlaProArgTyrLys 484
Db 1486 GTGGCCCTGAGAGAGCTGATGAAGCTGGCGCCCGGTACAAAGATGCCAGCACAAACAGC 1545
Qy 485 -----LeuGlyValHisGlyTyrAlaPheLe 493
Db 1546 AGGCCTAATGCGCCTCCACCTGGACTCTGGCAGCTTGGAGTGCACGGATACGCCTTTCT 1605
Qy 493 uAsnThrAsnAsnGlyTyrIleLeuSerHisProAspLeuArgProLeuTyrArgGluG 513
Db 1606 GAACACCAACAATGGGTACATCTCTCCATCCCGACCTCCGCGCCCTGTACAGAGAGGG 1665
Qy 513 YLysLysLeuLysProLysProAsnTyrAsnSerValAspLeuSerGluValGluTrpG 533
Db 1666 GAAGAACAATAAACCCAAACCTTAACACAGTGTGGATCTCTCCGAAGTGGAGTGGGA 1725
Qy 533 uAspGlnAlaGluSerLeuArgThrAlaMetIleAsnArgGluThrGlyThrLeuSerMe 553
Db 1726 AGACCAAGGCTGAATCTCTGAGAACAGCCATGATCAATAGGAAACAGGTACTCTCTCGAT 1785
Qy 553 tAspValLysValProMetAspLysGlyLysArgValLeuPheLeuThrAsnAspTyrPh 573
Db 1786 GGATGTGAAGGTTCGATGAAGGAAGCGAGTTCCTTCTGACCAATGACTACTT 1845
Qy 573 ePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArgGlyHisG 593
Db 1846 CTTTCAGGACATCAGCGACACCCCTTTCAGTTTGGGGTGGTGTCTCTCCGCGGCCACCG 1905
Qy 593 yGluTyrIleLeuLeuGlyAsnThrSerValGluGluGlyLeuHisAspLeuLeuHisPr 613
Db 1906 AGAATACATCTCTCTGGGNAACACGCTCTGTGAAAGAAGCGCTGCATGACTTGTCTCACCC 1965
Qy 613 oAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspProAspHisAr 633
Db 1966 AGACCTGGCCCTTGGCGCGTACTGGAATCTACTGCATCAGAGATATTGACCAAGACCCCG 2025
Qy 633 gLysLeuSerGlnLeuGluAlaMetIleArgPheLeuThrArgLysAspProAspLeuG 653
Db 2026 GAAGCTCGCCAGCTAGAGCCCATGATCGCTCTCCACAGGAAGAGCCACAGACCTGGA 2085
Qy 653 uCysAspGluGluLeuValArgGluValLeuPheAspAlaValThrAlaProMetG 673
Db 2086 GTG----- 2088
Qy 673 uAlaTyrTrpThrAlaLeuAlaLeuAsnMetSerGluGluSerGluHisValValAspMe 693
Db 2089 -----GAGTCTGAACACGTGGTGGACAT 2111
Qy 693 tAlaPheLeuGlyThrArgAlaGlyLeuLeuArgSerSerLeuPheValGlySerGlu 713
Db 2112 GGCTTCTTGGGCACCCCGGCTGGCTCTCTGAGAACGACGCTTGTTCGTGGGTCTCCAGAA 2171
Qy 713 sValSerAspArgLysPheLeuThrProGluAspGluAlaSerValPheThrLeuAspAr 733
Db 2172 GGTCTCCGACAGGAAGTTCTCTGACACCTGAGACGAGGCGCGGTGTTTCACTTGGACCG 2231

CC used in gene therapy. The present sequence is human TRICH12 cDNA

Sequence 4125 BP; 989 A; 1109 C; 1188 G; 839 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	4125
Score:	3808.00	Matches:	750
Percent Similarity:	80.90%	Conservative:	4
Best Local Similarity:	80.47%	Mismatches:	147
Query Match:	66.50%	Indels:	164
DB:	6	Gaps:	2

US-09-833-222A-10 (1-1090) x AAD22004 (1-4125)

Qy	11	AspArgValIysLeuTrpAlaAspThrPheGlyAspLeuTyrAsnThrValThrLys	30
Db	1120	GAACACGCTGAGCTATGGCGTGACACCTTCGGCGGGACCTGTATAACACTGTGACCAAA	1179
Qy	31	TyrSerGlySerLeuLeuGlnLysTyrLysAspValGluSerSerLeuLysIle	50
Db	1180	TACTCAGCTCTCTCTTGTCTGCAGACAGATACAAAGGATGTGGAGTCCAGTCTGAGATC	1239
Qy	51	GluGluValAspGlyLeuGluLeuValArgLysPheSerGluAspMetGluAsnMetLeu	70
Db	1240	GAGGAGGTGATGGCTTGGAGCTGGTGAGAAAGTTCTCAGAGGACATGGAGAACATGCTG	1299
Qy	71	ArgArgLysValGluAlaValGlnAsnLeuValGluAlaAlaGluGluAlaAspLeuAsn	90
Db	1300	CGAGGAAAGTCGAGCGCGTCCAGAACTCTGTGGAGCTCCGAGGAGGCCGACCTGAAC	1359
Qy	91	HisGluPheAsnGluSerLeuVal	98
Db	1360	CACGAATTCAATGAATCCCTGGTGGAACTTGGCGTGGGAGTTGGCGTGGGATGTCCGTG	1419
Qy	98	-----	98
Db	1420	ACGCAGTCCGGCGTGGGAGTTGGCGTGGGATGTCCGTACGCAGTCCGCGTGGGAGTT	1479
Qy	98	-----	98
Db	1480	GGCGTGGGATGTCCATAACCTGTCCGGCGTGGGAGTTGGCGTGGGATGTCCGTGAGG	1539
Qy	98	-----	98
Db	1540	CAGTCCGGCGTGGGAGTTGGCGTGGGATGTCCGTGACGCAGTCCGCGTGGGAGTTGGC	1599
Qy	98	-----	98
Db	1600	GTGGGATGTCCGTGACGCAGTCCGGCGTGGGAGTTGGCGTGGGATGTCCGTGAGGCAG	1659
Qy	98	-----	98
Db	1660	TCCGGCGTGGGAGTTGGCGTGGGATGTCCGTGACGCAGTCCGTGGGGGTTCCAGTGCC	1719
Qy	98	-----	98
Db	1720	CAGCGCGCCCGGGGTGTGTGTAGACTCATGGCCGCCCGGCCCTCTCTCG	1779
Qy	98	-----	98
Db	1780	TCCTCTCACCTGGCGGTTTCTCTTCTCTCTCCGCTGTCCGCGTGTCCGCGGCTGTCCGGCGGCC	1839
Qy	99	-----PheAspTyrTyrAsnSerValLeuIleAsnGlu	109
Db	1840	TCCGTGGGCTCACCCGCTCCACCCGATTCGACTATTACAACTCGGTCTGTATCAACAG	1899
Qy	110	ArgAspGluLysGlyAsnPheValGluLeuGluValaGluPheLeuLeuGluSerAsnAla	129
Db	1900	AGGACGAGAAAGGCAACTTCGTGGAGCTGGGGCGCCGAGTTCTCTCTGGAGTCCAATGCT	1959
Qy	130	HisPheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnVal	149
Db	1960	CACCTTCAGCAACTGCCGGTGAAACACTTCATCAGCAGCGTGCAGTGTGCCACCAACGTC	2019

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 03:09:42 ; Search time 171 Seconds
(without alignments)
2465.315 Million cell updates/sec

Title: US-09-833-222a-10
Perfect score: 5726
Sequence: 1 MAVALGTRRRDRVKLWADTF.....MPMNTVPVLLGGNIRVYAL 1090

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5726	100.0	1090	6	ABP59509 Human vol
2	5726	100.0	1090	7	ADF71820 Human cal
3	5386.5	94.1	1120	3	AAy92321 Human alp
4	5385.5	94.1	1207	7	ADe08021 Novel pro
5	5363	93.7	1097	4	AAu01038 Human sec
6	5363	93.7	1097	4	AB62262 Human cal
7	5276	92.1	1069	4	AAU01037 Human sec
8	5276	92.1	1069	4	AB62261 Human cal
9	5244.5	91.6	1096	3	AAy92324 Human alp
10	5234.5	91.4	1075	5	AAU09869 Novel hum
11	5230.5	91.3	1114	5	AAU09870 Novel hum
12	5179	90.4	1050	4	AAU01036 Human sec
13	5179	90.4	1050	4	AB62260 Human cal
14	4649	81.2	1096	3	AAy92323 Human alp
15	3808	66.5	1310	5	AAE13285 Human tra
16	3422	59.8	1091	5	AAE16666 Mouse cal
17	3419.5	59.7	1077	4	AAU01026 Human cal
18	3419.5	59.7	1077	4	AB62250 Human cal
19	3416.5	59.7	1091	5	AAE16665 Human cal
20	3410.5	59.6	1065	4	AAU01019 Human sec
21	3410.5	59.6	1085	3	AAy92320 Human alp
22	3410.5	59.6	1085	4	AAU01024 Human sec
23	3410.5	59.6	1085	4	AB62248 Human cal
24	3400.5	59.4	1071	4	AB62243 Human cal
25	3326.5	58.1	1038	4	AAU01018 Human sec

26	3326.5	58.1	1038	4	AB62242	Ab62242 Human cal
27	3278.5	57.3	1019	4	AAU01017	Aau01017 Human sec
28	3278.5	57.3	1019	4	AB62241	Ab62241 Human cal
29	3029.5	52.9	947	6	AB99658	Abb99658 Amino aci
30	2449	42.8	562	8	ADN33132	Adn33132 Human tra
31	2306	40.3	497	7	ADK40916	Adk40916 Novel hum
32	2306	40.3	497	8	ADR15609	Adr15609 Kinase 41
33	1870.5	32.7	519	3	AAy70460	Aay70460 Human mem
34	1792.5	31.3	350	4	AAU01022	Aau01022 Human sec
35	1792.5	31.3	350	4	AB62246	Ab62246 Human cal
36	1695	29.6	323	4	AAU01021	Aau01021 Human sec
37	1695	29.6	323	4	AB62245	Ab62245 Human cal
38	1598	27.9	304	4	AAU01020	Aau01020 Human sec
39	1598	27.9	304	4	AB62244	Ab62244 Human cal
40	1565	27.3	1258	8	ADO16905	Ado16905 Tobacco b
41	1554.5	27.1	1271	8	ADO16903	Ado16903 Tobacco b
42	1497.5	26.2	1215	4	AAE02340	Aae02340 D. melano
43	1410	24.6	2172	4	AB67958	Abb67958 Drosophil
44	1392.5	24.3	1245	8	ADO16901	Ado16901 Tobacco b
45	1322.5	23.1	1022	4	AB62234	Ab62234 Drosophil

ALIGNMENTS

RESULT 1
ABP59509
ID ABP59509 standard; protein; 1090 AA.
XX
AC ABP59509;
XX
DT 03-MAR-2003 (first entry)
XX
DE Human voltage gated calcium channel alpha2delta-4 subunit.

XX Human; voltage gated calcium channel; alpha2delta-4 subunit;
KW antiparkinsonian; tranquilizer; neuroprotective; anticonvulsant;
KW antimigraine; analgesic; cytostatic; antidepressant; antiinflammatory;
KW gene therapy; epilepsy; migraine; ataxia; vestibular defect;
KW chronic pain; neuropathic pain; Parkinson's disease; depression; cancer;
KW inflammation; seizure-related syndrome; anxiety; multiple sclerosis.
XX Homo sapiens.
XX WO200283947-A2.
XX
XX 24-OCT-2002.
XX
XX 10-APR-2002; 2002WO-US011297.
XX
XX 11-APR-2001; 2001US-00833222.
XX
XX (ORTH) ORTHO-MCNEIL PHARM INC.
XX
XX Qin N, Codd E;
XX
XX WPI; 2003-093006/08.
XX
XX N-PSDB; ABZ20598.
XX
XX New nucleic acid molecule encoding human alpha2 delta4 calcium channel
PT subunit protein, useful for diagnosing and treating a disease associated
PT with defects in the subunit protein, e.g. epilepsy, migraine, ataxia or
PT chronic pain.
XX
XX Claim 13; Page 56-59; 91pp; English.
XX
XX The present invention provides the protein and coding sequences of human
CC voltage gated calcium channel alpha2delta-4 subunit. The sequences are
CC useful for diagnosing and treating a disease or disorder associated with
CC a defective alpha2delta-4 subunit, such as seizure-related syndromes,
CC epilepsy, migraine, ataxia, vestibular defects, chronic pain, neuropathic
CC pain, mood, sleep interference, anxiety, ALS, multiple sclerosis, mania,
CC Parkinson's disease, substance abuse/addiction syndromes, depression,

CC	cancer, or inflammation. The present sequence is the protein of the	
CC	invention	
XX		
SQ	Sequence 1090 AA;	
	Query Match 100.0%; Score 5726; DB 6; Length 1090;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 1090; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 MAVALGTRRRDRVKLWADTGGDLVNTVTKYSGSLLLQKKYKDVESLKIIEVDGLVLR 60	
Db	1 MAVALGTRRRDRVKLWADTGGDLVNTVTKYSGSLLLQKKYKDVESLKIIEVDGLVLR 60	
Qy	61 KFSDEMNLRRKVEAQNLVEAAEADLNEHFNESLVFDYVNSVLINERDEKGNFVELG 120	
Db	61 KFSDEMNLRRKVEAQNLVEAAEADLNEHFNESLVFDYVNSVLINERDEKGNFVELG 120	
Qy	121 AEFLLSENAHFSNLPVNTSISSVOLPTNVYNKDPDILNGVYMSEALNAVVENFQRDPTL 180	
Db	121 AEFLLSENAHFSNLPVNTSISSVOLPTNVYNKDPDILNGVYMSEALNAVVENFQRDPTL 180	
Qy	181 TWQYFGSATGFFRIYPGIKWTPDENGVIITFCRNRGWYIOAATSPKDIVILVDVSGSMKG 240	
Db	181 TWQYFGSATGFFRIYPGIKWTPDENGVIITFCRNRGWYIOAATSPKDIVILVDVSGSMKG 240	
Qy	241 LRWTIAKHTITTTLDLTGENDFVNI IAYNDYVHYIEPCFKGILVQADRDNRHFLLVEE 300	
Db	241 LRWTIAKHTITTTLDLTGENDFVNI IAYNDYVHYIEPCFKGILVQADRDNRHFLLVEE 300	
Qy	301 LMVKGVGVDQALREAFQILKQFEAKQGSCLNQAIMLISDGAVEDYEPVFEKYNPDCK 360	
Db	301 LMVKGVGVDQALREAFQILKQFEAKQGSCLNQAIMLISDGAVEDYEPVFEKYNPDCK 360	
Qy	361 VRVFTYILIGREVSFADRMKIACNKGYYTQISTLADTQENVMEYLHLVSRPVIINHDD 420	
Db	361 VRVFTYILIGREVSFADRMKIACNKGYYTQISTLADTQENVMEYLHLVSRPVIINHDD 420	
Qy	421 IIWTEAYMDSKLLSSQAQSITLTTVAMPVFSKNETRSHGILLGVGSDVALRELKMLA 480	
Db	421 IIWTEAYMDSKLLSSQAQSITLTTVAMPVFSKNETRSHGILLGVGSDVALRELKMLA 480	
Qy	481 PRYKLGHVGFALNTNNGYITLHPDLRLPLRYREGKKLKPKNYNSVDLSEVWEQAEASLR 540	
Db	481 PRYKLGHVGFALNTNNGYITLHPDLRLPLRYREGKKLKPKNYNSVDLSEVWEQAEASLR 540	
Qy	541 TAMINRETGLSDVKVPMDKGRVLPFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGN 600	
Db	541 TAMINRETGLSDVKVPMDKGRVLPFLTNDYFFTDISDTPFSLGAVLSRGHGEYILLGN 600	
Qy	601 TSVEEGLHDLHPDLALAGDWIYCITDIDPHRKLSQLLEAMIRFLTRKDPDLSCDEELVR 660	
Db	601 TSVEEGLHDLHPDLALAGDWIYCITDIDPHRKLSQLLEAMIRFLTRKDPDLSCDEELVR 660	
Qy	661 EVLFDVAVTAPMEAYMTALANMSESESHVVDMAFLGTRAGLLRSSLFVSGSEKVSQRKFL 720	
Db	661 EVLFDVAVTAPMEAYMTALANMSESESHVVDMAFLGTRAGLLRSSLFVSGSEKVSQRKFL 720	
Qy	721 TPDEASVFTLDRPFLMYROASHPAGSFVFNLRWAEGPESAGEPMVVTASTAVATVDK 780	
Db	721 TPDEASVFTLDRPFLMYROASHPAGSFVFNLRWAEGPESAGEPMVVTASTAVATVDK 780	
Qy	781 RTAIAAAGVQMKLEFLQRFKFAATROCSVDGPGYPTQSCDSDDLDCFVIDNNGFILLISKR 840	
Db	781 RTAIAAAGVQMKLEFLQRFKFAATROCSVDGPGYPTQSCDSDDLDCFVIDNNGFILLISKR 840	
Qy	841 SRTGRFLRGVDGAVLTQLLSMGVFSQVTMYDYOAMCKPSSHHSAAQPLVSPISAPLTA 900	
Db	841 SRTGRFLRGVDGAVLTQLLSMGVFSQVTMYDYOAMCKPSSHHSAAQPLVSPISAPLTA 900	
Qy	901 TRWLLOELVLFLEWSVWGSDRGAEAKSVFHHSHKHKQDPLQCDTEYPVFNVPQAI 960	
Db	901 TRWLLOELVLFLEWSVWGSDRGAEAKSVFHHSHKHKQDPLQCDTEYPVFNVPQAI 960	

Qy	961 REANGIVEGCPCKQVFWQOIPNSNLLLLVTDPTCDSCSPFPVLPQATEVKYNASVKCDR 1020	
Db	961 REANGIVEGCPCKQVFWQOIPNSNLLLLVTDPTCDSCSPFPVLPQATEVKYNASVKCDR 1020	
Qy	1021 MRSQKLRRRPDSCHAFHPEVRVEADRGWAGFSFSPNPLCLGLCPCROEHIGMPNTPVPVL 1080	
Db	1021 MRSQKLRRRPDSCHAFHPEVRVEADRGWAGFSFSPNPLCLGLCPCROEHIGMPNTPVPVL 1080	
Qy	1081 LGGNIRVYAL 1090	
Db	1081 LGGNIRVYAL 1090	
	RESULT 2	
	ADP71820	
ID	ADP71820 standard; protein; 1090 AA.	
XX		
AC	ADP71820;	
XX		
DT	12-FEB-2004 (first entry)	
DE	Human calcium channel alpha2delta4 subunit.	
XX		
KW	neuroprotective; cytosstatic; gene therapy; calcium channel;	
KW	alpha2delta-4; amyotrophic lateral sclerosis; multiple sclerosis; cancer;	
XX	human.	
OS	Homo sapiens.	
XX		
PN	US2003170785-A1.	
XX		
PD	11-SEP-2003.	
XX		
PF	10-APR-2002; 2002US-00119624.	
XX		
PR	11-APR-2001; 2001US-00833222.	
XX		
PA	{QINN/} QIN N.	
PA	{CODD/} CODD E.	
XX		
PI	Qin N, Codd E;	
XX		
DR	WPI; 2003-898262/82.	
DR	N-PSDB; ADP71819.	
XX		
PT	New human alpha2 delta4 calcium channel subunit protein and nucleic acid	
PT	molecule, useful for diagnosing and treating diseases associated with	
PT	defective calcium channel subunit, e.g. cancer and multiple sclerosis.	
XX		
PS	Claim 17; SEQ ID NO 10; 37pp; English.	
XX		
CC	The invention describes a new isolated and purified nucleic acid molecule	
CC	comprising: a sequence having at least a 70% identity to nucleotides 1-	
CC	224 or 3308-3486 of a sequence of 3486 bp (S1) fully defined in the	
CC	specification; at least 15 sequential bases of the polynucleotide of (a);	
CC	or a sequence that is complementary to the polynucleotide of (a) or (b).	
CC	Specifically claimed is an alpha2delta-4 nucleic acid molecule comprising	
CC	a sequence of 3486 bp fully defined in the specification and encoding an	
CC	alpha2delta-4 calcium channel subunit protein having a sequence of 1090	
CC	amino acids fully defined in the specification. The nucleic acid molecule	
CC	and polypeptide are useful in diagnosing and treating a disease or	
CC	disorder associated with a defective alpha2delta-4 subunit, such as	
CC	amyotrophic lateral sclerosis, multiple sclerosis or cancer. The methods	
CC	may be used for identifying compounds capable of treating the above-	
CC	mentioned diseases or disorders. This is the amino acid sequence of human	
CC	calcium channel alpha2delta-4 subunit.	
XX		
SQ	Sequence 1090 AA;	
	Query Match 100.0%; Score 5726; DB 7; Length 1090;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 1090; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

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Qy 1 MAVALGTRRRDRVKLWADTFGGDLVNTVTYKYSGLLQKKYKDVESLSKIEEVDGLVLR 60
Db 1 MAVALGTRRRDRVKLWADTFGGDLVNTVTYKYSGLLQKKYKDVESLSKIEEVDGLVLR 60

Qy 61 KPSEDMENLRRKVEAVQNLVEAAEADLNHERNESLVFDYNSVLNERDEKGNFVELG 120
Db 61 KPSEDMENLRRKVEAVQNLVEAAEADLNHERNESLVFDYNSVLNERDEKGNFVELG 120

Qy 121 AEFLLESNAHFSNLPVNTSISSVQLPTNVYNKOPDILNGVYMSALNAVFVENFQRPDPTL 180
Db 121 AEFLLESNAHFSNLPVNTSISSVQLPTNVYNKOPDILNGVYMSALNAVFVENFQRPDPTL 180

Qy 181 TWQYFGSATGFFRIYPGIKWTPDENGUITPDCNRGHWIQAATSPKIDIVILDVSGSMKG 240
Db 181 TWQYFGSATGFFRIYPGIKWTPDENGUITPDCNRGHWIQAATSPKIDIVILDVSGSMKG 240

Qy 241 LRMTIAKHITITLDTLGENDFVNI IAYNDVYHIEPCFKGILVQADRDNRHFKLLAVEE 300
Db 241 LRMTIAKHITITLDTLGENDFVNI IAYNDVYHIEPCFKGILVQADRDNRHFKLLAVEE 300

Qy 301 LMVKGVGVPDQALREAFQILKQFEAKQGSILCNQAIMLISDGAVEDYEPVEKYNWPDCK 360
Db 301 LMVKGVGVPDQALREAFQILKQFEAKQGSILCNQAIMLISDGAVEDYEPVEKYNWPDCK 360

Qy 361 VRVPTYLIGREVSPADRMKWIACNNKGYITQISTLADTQENVMYHLVSRPMVINHDHD 420
Db 361 VRVPTYLIGREVSPADRMKWIACNNKGYITQISTLADTQENVMYHLVSRPMVINHDHD 420

Qy 421 IITEAYWDSKLLSSQAQSLTLTTVAMPVFSKNETRSHGILLGVVGSVDVALRELKLA 480
Db 421 IITEAYWDSKLLSSQAQSLTLTTVAMPVFSKNETRSHGILLGVVGSVDVALRELKLA 480

Qy 481 PRYKLGVHGVAFLNTNNGYILSHPDRLPLREGKLLKPKPNYSVDLSEWEDQAESLR 540
Db 481 PRYKLGVHGVAFLNTNNGYILSHPDRLPLREGKLLKPKPNYSVDLSEWEDQAESLR 540

Qy 541 TMINRETGILSMVKVPMQKGRVLFNTDYPFTDISDTPFSLGAVLSRGHGYYILLGN 600
Db 541 TMINRETGILSMVKVPMQKGRVLFNTDYPFTDISDTPFSLGAVLSRGHGYYILLGN 600

Qy 601 TSVEEGLHLLHPDALAGDWIYICITDIDPHRKLQLEAMIRFLTRKDPDLECDLVR 660
Db 601 TSVEEGLHLLHPDALAGDWIYICITDIDPHRKLQLEAMIRFLTRKDPDLECDLVR 660

Qy 661 EVLFDVAVTAPMEAYWTALALNSEESEHVVDMAFLGTRAGLLRSSLFVGSSEKVS DRKFL 720
Db 661 EVLFDVAVTAPMEAYWTALALNSEESEHVVDMAFLGTRAGLLRSSLFVGSSEKVS DRKFL 720

Qy 721 TPDEASVFTLDRPPLMYROASEHPAGSFVFNLRWAGSPSAGBPMVVTASTAVAVTDK 780
Db 721 TPDEASVFTLDRPPLMYROASEHPAGSFVFNLRWAGSPSAGBPMVVTASTAVAVTDK 780

Qy 781 RTAIAAAGVQMKLEFLQRFKFAATROCSTVDGPTYTQSCDSDLDLCFVINDNGFILLISK 840
Db 781 RTAIAAAGVQMKLEFLQRFKFAATROCSTVDGPTYTQSCDSDLDLCFVINDNGFILLISK 840

Qy 841 SRETGRFLGVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSHHSSAAQPLVSPISAFITA 900
Db 841 SRETGRFLGVDGAVLTQLLSMGVFSQVTMYDYQAMCKPSHHSSAAQPLVSPISAFITA 900

Qy 901 TRWLLQLVLFLLEWSVWGSDYRGAEAKSVFHHSHKHKKQDPLQPCDTEYFPVYQPAI 960
Db 901 TRWLLQLVLFLLEWSVWGSDYRGAEAKSVFHHSHKHKKQDPLQPCDTEYFPVYQPAI 960

Qy 961 REANGIECGPCQKVFVVQIIPNSNLLLLTDPDTCDCSI PPPVLQAEATEVKYNASVKCDR 1020
Db 961 REANGIECGPCQKVFVVQIIPNSNLLLLTDPDTCDCSI PPPVLQAEATEVKYNASVKCDR 1020

Qy 1021 MRSQKLRRRPPDSCHAFPEVRVEADRGWAGFSSPNPLCLGICPCQRBHIGMPMNTPPVVL 1080
Db 1021 MRSQKLRRRPPDSCHAFPEVRVEADRGWAGFSSPNPLCLGICPCQRBHIGMPMNTPPVVL 1080

Qy 1081 LGGNIRVYAL 1090
```

Db 1081 LGGNIRVYAL 1090

RESULT 3

AA92321 ID AAY92321 standard; protein; 1120 AA.

XX AAY92321;

XX 10-AUG-2000 (first entry)

XX Human alpha-2-delta-D calcium channel subunit.

XX alpha-2-delta-D; calcium channel subunit; 3p21.1; gabapentin; cytostatic;
XX anticonvulsant; antimigrane; antiparkinsonian; antidepressant.

OS Homo sapiens.

XX WO2000020450-A2.

XX 13-APR-2000.

XX 07-OCT-1999; 99WO-US023519.

XX 07-OCT-1998; 98US-0103322P.

XX 30-OCT-1998; 98US-0106473P.

XX 29-DEC-1998; 98US-0114088P.

XX (WARN) WARNER LAMBERT CO.

XX Johns MA, Moldover B, Offord JD;

XX WPI; 2000-303744/26.

XX N-PSDB; AAA09254.

XX New human nucleic acids encoding the alpha2delta-C and alpha2delta-D

XX anxiety, multiple sclerosis or cancer.

XX Claim 8; Page 67; 88pp; English.

XX The alpha-2-delta-D gene encodes a calcium channel subunit polypeptide.

XX The gene has been mapped to chromosome 12p13.1. This gene and the related

XX alpha-2-delta-C and -B genes are useful for protecting mammalian cells

XX from abnormal calcium flux by introducing expression vectors containing

XX the respective gene into mammalian cells. The antisense genes are also

XX useful for treating or preventing epilepsy. The alpha-delta-2-A protein

XX is a high-affinity binding target of the anti-convulsant drug gabapentin.

XX Therefore, alpha-delta-2 proteins may also be targeted to treat seizure-

XX related syndromes, migraine, ataxia, vestibular defects, chronic pain,

XX sleep interference, anxiety, amyotrophic lateral sclerosis (ALS), multiple

XX sclerosis, mania, tremor, parkinsonism, substance abuse or addiction

XX syndromes, mood, depression or cancer

SQ Sequence 1120 AA;

Query Match 94.1%; Score 5386.5; DB 3; Length 1120;

Best Local Similarity 98.0%; Pred. No. 0;

Matches 1033; Conservative 5; Mismatches 13; Indels 3; Gaps 2;

Qy 11 DRVKLWADTFGGDLVNTVTYKYSGLLQKKYKDVESLSKIEEVDGLVLRKFSDEMML 70

Db 58 ETVKLWADTFGGDLVNTVTYKYSGLLQKKYKDVESLSKIEEVDGLVLRKFSDEMML 117

Qy 71 RRKVEAVQNLVEAAEADLNHERNESLVFDYNSVLNERDEKGNFVELCAEFLLSENAH 130

Db 118 RRKVEAVQNLVEAAEADLNHERNESLVFDYNSVLNERDEKGNFVELCAEFLLSENAH 177

Qy 131 FSNLPVNTSISSVQLPTNVYNKOPDILNGVYMSALNAVFVENFQRPDPTLTWQYFGSATG 190

Db 178 FSNLPVNTSISSVQLPTNVYNKOPDILNGVYMSALNAVFVENFQRPDPTLTWQYFGSATG 237


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Db 505 EVSFADRMKWTACNNKGYITQISTLADTQENVMEYLVHLSRPMVINHDHDIITWEAYMDS 564
Qy 431 KLLSSQASQLTLLTTVAMPVFSKKNETSRSHGILLGVGSDVALRELKMLAPRYKLGHVHG 490
Db 565 KLLSSQASQLTLLTTVAMPVFSKKNETSRSHGILLGVGSDVALRELKMLAPRYKLGHVHG 624
Qy 491 AFLNTNNGYILSHDPDLAPLREGKLLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 550
Db 625 AFLNTNNGYILSHDPDLAPLREGKLLKPKPNYNSVDLSEVEWEDQAESLRTAMINRETGT 684
Qy 551 LSMVKVPMKDKRVLFTNDYFTDIDSDTPFSLGAVLSRCHGYIILGNITSVEEGLHDL 610
Db 685 LSMVKVPMKDKRVLFTNDYFTDIDSDTPFSLGAVLSRCHGYIILGNITSVEEGLHDL 744
Qy 611 LHPDLALAGDWIYICITIDPDHRLKLSQLEAMIRFLTRKDPDLECDLBEVLREVLFDVVTA 670
Db 745 LHPDLALAGDWIYICITIDPDHRLKLSQLEAMIRFLTRKDPDLECDLBEVLREVLFDVVTA 804
Qy 671 PMEAYWTALALNMSESEHVVDMAPLGTAGLLRSSLFVGSEKVSDRKFLTPDEASVFT 730
Db 805 PMEAYWTALALNMSESEHVVDMAPLGTAGLLRSSLFVGSEKVSDRKFLTPDEASVFT 864
Qy 731 LDRPPLVROASHPAGSFVFNLRWAGSPESAGPMMVVTASTAVAVTVDKRTAIAAAGV 790
Db 865 LDRPPLVROASHPAGSFVFNLRWAGSPESAGPMMVVTASTAVAVTVDKRTAIAAAGV 924
Qy 791 QMKLEFLQRKFWAATRCQSTVDGPTQSCSDSDLDLDCFVINDNNGFILSKRSRETGRFLGE 850
Db 925 QMKLEFLQRKFWAATRCQSTVDGPTQSCSDSDLDLDCFVINDNNGFILSKRSRETGRFLGE 984
Qy 851 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHSAAQPLVSPISAFLTATRWLLQBLVL 910
Db 985 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHSAAQPLVSPISAFLTATRWLLQBLVL 1044
Qy 911 FLLEWSVWGSWYDRGAESKSVFHHSHKHKKDPLQPCDTEPVPVYQPAIREANGIVECG 970
Db 1045 FLLEWSVWGSWYDRGAESKSVFHHSHKHKKDPLQPCDTEPVPVYQPAIREANGIVECG 1104
Qy 971 PCQKRVFVQIQPNSNLLLLVTDPTCDGCSIFPPVLQEAATEVKYNASVKCDRMRSQKLRPP 1030
Db 1105 PCQKRVFVQIQPNSNLLLLVTDPTCDGCSIFPPVLQEAATEVKYNASVKCDRMRSQKLRPP 1164
Qy 1031 DSCHAFHPEVVRVADRQWAGFSSNP--LCIGLC 1062
Db 1165 DSCHAFHPEVVRVADRQWAGFSSNP--LCIGLC 1197

RESULT 5
AAU01038
XX AAU01038 standard; protein; 1097 AA.
AC AAU01038;
XX
DT 04-JUL-2001 (first entry)
XX
DE Human secreted soluble alpha2delta calcium channel subunit #18 protein.
XX
KW Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;
KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;
KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;
KW filter binding assay; wheat germ lectin flashplate assay.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT Misc-difference 747..749 /note= "Encoded by GCTGCG"
FT FT
FT Misc-difference 763..764 /note= "Encoded by TCCGAGTGCCTCTCGAGACGAG
FT FT CTTGCTGCTGCTCGAGAGGCTCCGAC"
XX
PN W0200119870-A2.
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XX 22-MAR-2001.
XX 18-SEP-2000; 2000WO-EP009137.
XX 16-SEP-1999; 99US-00397550.
XX (WARN ) WARNER LAMBERT CO.
XX Brown JP, Bertelli F;
XX WPI; 2001-235262/24.
XX N-PSDB; AAS01433.
XX Calcium channel alpha2delta subunits, useful in e.g. SPA assays,
XX Flashplate assays, Nickel Flashplate assays, Filter binding assays or
XX Wheat Germ Lectin Flashplate assays.
XX Claim 27; Page 156-160; 160pp; English.
XX The present sequence represents human secreted calcium channel
XX alpha2delta subunit #18 which is soluble and retains the functional
XX characteristics of the full length or wild type alpha2delta subunit
XX (AAU01025) from which it is derived. The invention relates to truncated
XX alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins
XX which retain their affinity for radioactively labelled gabapentin. The
XX alpha2delta subunit is 1 of the components of the heteromultimeric
XX voltage-dependent calcium channel (VDCC) complexes present in neuronal
XX and non-neuronal tissues including heart and skeletal muscle. Numerous
XX soluble forms of the human calcium channel alpha2delta subunits (AAU01014
XX -AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the porcine
XX calcium channel alpha2delta subunits (AAU01027-AAU01031) are described.
XX The secreted soluble alpha2delta subunit may be used in assays e.g.
XX scintillation proximity assay (SPA), flashplate, nickel flashplate,
XX filter binding or wheat germ lectin flashplate assays to detect or
XX measure the binding or interaction of a ligand (e.g. gabapentin, L-
XX Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine, L-
XX Valine, Spermine and/or L-Phenylalanine) of a calcium channel alpha2delta
XX subunit
XX SQ Sequence 1097 AA;
XX
Query Match 93.7%; Score 5363; DB 4; Length 1097;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1028; Conservative 2; Mismatches 8; Indels 2; Gaps 2;
Qy 11 DRVKLWADTFGGDLVNTVTYKSGSLLLQKKYKDVESLKIIEVDGLBLVRKFSDMENML 70
Db 58 ETVKLWADTFGGDLVNTVTYKSGSLLLQKKYKDVESLKIIEVDGLBLVRKFSDMENML 117
Qy 71 RRKVEAVQNIVEAAEADLNHEFNESLVFDYNSVLINERDEKGNFVELGAEFLLESNAH 130
Db 118 RRKVEAVQNIVEAAEADLNHEFNESLVFDYNSVLINERDEKGNFVELGAEFLLESNAH 177
Qy 131 FSNLPVNTSISVOLPTNVNKKDPDILNGVYMSALNAVVFENFQDPTLTWQYFGSATG 190
Db 178 FSNLPVNTSISVOLPTNVNKKDPDILNGVYMSALNAVVFENFQDPTLTWQYFGSATG 237
Qy 191 FFRIYPGIKWTPDENGVIITFDCRNRGWYIQAATSPKDIIVLDVSGSMKGLRMTIAKHTI 250
Db 238 FFRIYPGIKWTPDENGVIITFDCRNRGWYIQAATSPKDIIVLDVSGSMKGLRMTIAKHTI 297
Qy 251 TTILDTLGENDFNIIAYNDYVHYIEPCFGLVQADRDNRHFKLLVEELMVKGVGVD 310
Db 298 TTILDTLGENDFNIIAYNDYVHYIEPCFGLVQADRDNRHFKLLVEELMVKGVGVD 357
Qy 311 QALREAFQILKQFOEAKQKSLCNQAIMLISDGAVEDYEPVEKYNWPCDKVRVFTYLIGR 370
Db 358 QALREAFQILKQFOEAKQKSLCNQAIMLISDGAVEDYEPVEKYNWPCDKVRVFTYLIGR 417
Qy 371 EVSFADRMKWTACNNKGYITQISTLADTQENVMEYLVHLSRPMVINHDHDIITWEAYMDS 430
Db 418 EVSFADRMKWTACNNKGYITQISTLADTQENVMEYLVHLSRPMVINHDHDIITWEAYMDS 477
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QY	431	KLLSSQAQSLTLTLTTVAMPVFSKKNETRSHGILLGVGSDVALRELKMLAPRYKLGVHG	490
Db	478	KLLSSQAQSLTLTLTTVAMPVFSKKNETRSHGILLGVGSDVALRELKMLAPRYKLGVHG	537
QY	491	AFLNTNNGYILSHPDRLPLVREGKLLKPKPNVNSVDLSEVWEQOAESLRTAMINRETGT	550
Db	538	AFLNTNNGYILSHPDRLPLVREGKLLKPKPNVNSVDLSEVWEQOAESLRTAMINRETGT	597
QY	551	LSMDVKVPMDKGRKVLFLTNDYFFTDIDSTPFSLGAVLSRGHGEYIILGNTSVBEGHLDL	610
Db	598	LSMDVKVPMDKGRKVLFLTNDYFFTDIDSTPFSLGAVLSRGHGEYIILGNTSVBEGHLDL	657
QY	611	LHPDLALAGDMYICITDIDPHRKLSQLEAMIRFLTRKDPDLECEDELVRVFLDAVVTA	670
Db	658	LHPDLALAGDMYICITDIDPHRKLSQLEAMIRFLTRKDPDLECEDELVRVFLDAVVTA	717
QY	671	PMEAYWTALALNMSESESHVVDMAPLGTGA-GLLRSSLFVGSEKVSORKFLTPTDEASVF	729
Db	718	PMEAYWTALALNMSESESHVVDMAPLGTGRASGLLRSSLFVGSEKVSORKFLTPTDEASVF	777
QY	730	TLDKRPFLWYRQASEHPAGSFVFNLRWABGPESAGEPMVVTASTAVAVTVDKRTAIAAAG	789
Db	778	TLDKRPFLWYRQASEHPAGSFVFNLRWABGPESAGEPMVVTASTAVAVTVDKRTAIAAAG	837
QY	790	VQMKLEFLQRFKWAATRCSTVDGPYTCQSCDSLDLCFVIDNNGFILLISKRSRETGRFLG	849
Db	838	VQMKLEFLQRFKWAATRCSTVDGPCTQSCDSLDLCFVIDNNGFILLISKRSRETGRFLG	897
QY	850	EVDGAVLTQLLSMGVFSQVTTYDYQAMCKPSSHHSAAQPLVSPISAFLATRWLLQELV	909
Db	898	EVDGAVLTQLLSMGVFSQVTTYDYQAMCKPSSHHSAAQPLVSPISAFLATRWLLQELV	957
QY	910	LFLLEWSVMGWSYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFTVQPAIREANGIVEC	969
Db	958	LFLLEWSVMGWSYDRGAEAKSVFHHSHKHKKQDPLQPCDTEYPVFTVQPAIREANGIVEC	1017
QY	970	GPCQKVFVVQIQPNSNLLLVTDPTDCDSIFPPVLQEADEVKYNASVKCDMRMSQKLRRR	1029
Db	1018	GPCQKVFVVQIQPNSNLLLVTDPTDCDSIFPPVLQEADEVKYNASVKCDMRMSQKLRRR	1077
QY	1030	PDSCHAFHPVRVEADRGWA 1049	
Db	1078	PDSCHAFHPREENAQ-DCGGA 1096	
RESULT 6			
AAB62262			
ID	AAB62262 standard; protein; 1097 AA.		
XX	AAB62262;		
XX	11-JUN-2001 (first entry)		
DE	Human calcium channel alpha2delta subunit.		
KW	Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;		
KW	nervous system disorder; pain; epilepsy; anxiety; human.		
OS	Homo sapiens.		
XX	WO200120336-A2.		
XX	22-MAR-2001.		
XX	18-SEP-2000; 2000WO-EP009136.		
PR	16-SEP-1999; 99US-00397549.		
XX	(WARN) WARNER LAMBERT CO.		
XX	Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;		

Qy 671 PMAEYWTALANMSESEHVVDMFLGTRA-GLLRSSLFVGSEKVSQDRKFLTPDEASVF 729
Db 718 PMAEYWTALANMSESEHVVDMFLGTRASGLLRSSLFVGSEKVSQDRKFLTPDEASVF 777
Qy 730 TLDREPLWYQASEHPAGSFVNLRWAGSPESAGEPMVVTASTAVAVTVDKRTAIAAAG 789
Db 778 TLDREPLWYQASEHPAGSFVNLRWAGSPESAGEPMVVTASTAVAVTVDKRTAIAAAG 837
Qy 790 VQMKLEFLQKFWAATRCQSTVDGPTQSCEDSDLDLCFVIDNNGFILLISKRSTRETGRFLG 849
Db 838 VQMKLEFLQKFWAATRCQSTVDGPTQSCEDSDLDLCFVIDNNGFILLISKRSTRETGRFLG 897
Qy 850 EVDGAVLTQLLSMGVFSQVMTYDYQAMCKPSSHHSAAQPLVSPISAFLTATRWLLQELV 909
Db 898 EVDGAVLTQLLSMGVFSQVMTYDYQAMCKPSSHHSAAQPLVSPISAFLTATRWLLQELV 957
Qy 910 LFLLEWSVGSWYDRGAEAKSVFHHSHKHKQDPLOCDTEYFVYVQPAIRREANGIVEC 969
Db 958 LFLLEWSVGSWYDRGAEAKSVFHHSHKHKQDPLOCDTEYFVYVQPAIRREANGIVEC 1017
Qy 970 GPCQKVFVWQOIPNSNLLLVTDPTCDCSIFPPVLQATEVKYNASVKCDRMSQKLRRR 1029
Db 1018 GPCQKVFVWQOIPNSNLLLVTDPTCDCSIFPPVLQATEVKYNASVKCDRMSQKLRRR 1077
Qy 1030 PDSCHAFHPPEVRVEADRGWA 1049
Db 1078 PDSCHAFHPPENAQ-DCGGA 1096

RESULT 7

ID AAU01037 standard; protein; 1069 AA.
XX AC AAU01037;
XX DT 04-JUL-2001 (first entry)
XX DE Human secreted soluble alpha2delta calcium channel subunit #17 protein.
XX KW Human; secreted calcium channel alpha2delta subunit; alpha2delta-2;
XX KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;
XX KW gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;
XX KW filter binding assay; wheat germ lectin flashplate assay.
XX OS Homo sapiens.
XX OS WO200119870-A2.
XX PN 22-MAR-2001.
XX PD 18-SEP-2000; 2000WO-EP009137.
XX PF 16-SEP-1999; 99US-00397550.
XX PR (WARN) WARNER LAMBERT CO.
XX PA Brown JP, Bertelli F;
XX PI WPI; 2001-235262/24.
XX DR N-PSDB; AAS01432.

XX Calcium channel alpha2delta subunits, useful in e.g. SPA assays,
XX PT Flashplate assays, Nickel Flashplate assays, Filter binding assays or
XX PT Wheat Germ Lectin Flashplate assays.
XX PS Claim 28; Page 153-156; 160pp; English.
XX CC The present sequence represents human secreted calcium channel
XX CC alpha2delta subunit #17 which is soluble and retains the functional
XX CC characteristics of the full length or wild type alpha2delta subunit
XX CC (AAU01025) from which it is derived. The invention relates to truncated
XX CC alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins
XX CC which retain their affinity for radioactively labelled gabapentin. The

CC alpha2delta subunit is 1 of the components of the heteromultimeric
CC voltage-dependent calcium channel (VDCC) complexes present in neuronal
CC and non-neuronal tissues including heart and skeletal muscle. Numerous
CC soluble forms of the human calcium channel alpha2delta subunits (AAU01014
CC -AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the porcine
CC calcium channel alpha2delta subunits (AAU01027-AAU01031) are described.
CC The secreted soluble alpha2delta subunit may be used in assays e.g.
CC scintillation proximity assay (SPA), flashplate, nickel flashplate,
CC filter binding or wheat germ lectin flashplate assays to detect or
CC measure the binding or interaction of a ligand (e.g. gabapentin, L-
CC Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine, L-
CC Valine, Spermine and/or L-Phenylalanine) of a calcium channel alpha2delta
CC subunit.
XX Sequence 1069 AA;

Query Match 92.1%; Score 5276; DB 4; Length 1069;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1008; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 11 DRVKLWADTFGGDLVNTVTYKSGSLLLQKKYKDVESLKIIEVDGLBLVRKFSDEMNM 70
Db 58 ETVKLWADTFGGDLVNTVTYKSGSLLLQKKYKDVESLKIIEVDGLBLVRKFSDEMNM 117
Qy 71 RRKVEAVQNIVEAAEADLNHEFNEISLVFDYNSVLINERDEKGNFVGLGAEFLLENAH 130
Db 118 RRKVEAVQNIVEAAEADLNHEFNEISLVFDYNSVLINERDEKGNFVGLGAEFLLENAH 177
Qy 131 FSNLPVNTSISVOLPTNVYKDPDILNGVYMGSEALNAVFNQDRPTLTWQYFGSATG 190
Db 178 FSNLPVNTSISVOLPTNVYKDPDILNGVYMGSEALNAVFNQDRPTLTWQYFGSATG 237
Qy 191 FFRYPGKWTDPDENGVIPTDCRNRGWYIOAATSPKDIVILVDVSGSMKGLRMTIAKHTI 250
Db 238 FFRYPGKWTDPDENGVIPTDCRNRGWYIOAATSPKDIVILVDVSGSMKGLRMTIAKHTI 297
Qy 251 TTILDTLGENDFNIIAYNDYVHYIEPCFKGILVQADRDNRHFKLVEELMVKGVGVVD 310
Db 298 TTILDTLGENDFNIIAYNDYVHYIEPCFKGILVQADRDNRHFKLVEELMVKGVGVVD 357
Qy 311 QALREAFQILKQFOEAKQKQSLCNOAIMLISDGAVEDYEPVEFKYNWPDCKVRVFTYLIGR 370
Db 358 QALREAFQILKQFOEAKQKQSLCNOAIMLISDGAVEDYEPVEFKYNWPDCKVRVFTYLIGR 417
Qy 371 EVSFADRMKWIACNNKGYTQISTLADTQBNVMEYHLVLSRPMVINHDHDIITWEAYMDS 430
Db 418 EVSFADRMKWIACNNKGYTQISTLADTQBNVMEYHLVLSRPMVINHDHDIITWEAYMDS 477
Qy 431 KLLSSQAQSLTLTTVAMPVFSKKNETRSKILGVVGSVALBELMKLAPRYKLGVHG 490
Db 478 KLLSSQAQSLTLTTVAMPVFSKKNETRSKILGVVGSVALBELMKLAPRYKLGVHG 537
Qy 491 AFLNTNNGYILSHPDRLPLVREGKCLKPKPNYNSVDLSEVEDQAESLRTAMINRETGT 550
Db 538 AFLNTNNGYILSHPDRLPLVREGKCLKPKPNYNSVDLSEVEDQAESLRTAMINRETGT 597
Qy 551 LSMDEVKVPMDKGRVLFNTNDYFPTDISDPFSLGAVLSRGHGEYILLGNNTSVEEGLHDL 610
Db 598 LSMDEVKVPMDKGRVLFNTNDYFPTDISDPFSLGAVLSRGHGEYILLGNNTSVEEGLHDL 657
Qy 611 LHPDLALAGDWIYCIITDIDPDHRLKSOLEAMIRFLTRKDPDLCDLREVLFPDVAVTA 670
Db 658 LHPDLALAGDWIYCIITDIDPDHRLKSOLEAMIRFLTRKDPDLCDLREVLFPDVAVTA 717
Qy 671 PMAEYWTALANMSESEHVVDMFLGTRAGLRSSLFVGSEKVSQDRKFLTPDEASVFT 730
Db 718 PMAEYWTALANMSESEHVVDMFLGTRAGLRSSLFVGSEKVSQDRKFLTPDEASVFT 777
Qy 731 LDRFPLWYQASEHPAGSFVNLRWAGSPESAGEPMVVTASTAVAVTVDKRTAIAAAGV 790
Db 778 LDRFPLWYQASEHPAGSFVNLRWAGSPESAGEPMVVTASTAVAVTVDKRTAIAAAGV 837
Qy 791 QMKLEFLQKFWAATRCQSTVDGPTQSCEDSDLDLCFVIDNNGFILLISKRSTRETGRFLGE 850

Db 838 QMKLEFLQRFWAATRCSTVDGCTQSCSDSLDCFDVNNNGFILSKSRSTGRFLGE 897
 Qy 851 VDGAULTQLLSMGVFSQVWYDYQAMCKPSSHHSAAQPLVSPISAFELTATRWLLQELVL 910
 Db 898 VDGAULTQLLSMGVFSQVWYDYQAMCKPSSHHSAAQPLVSPISAFELTATRWLLQELVL 957
 Qy 911 FLEWSVMGWDYRGAEAKSVFHHSHKHKQDPLQPCDTBYPVYQPAIREANGIVECG 970
 Db 958 FLEWSVMGWDYRGAEAKSVFHHSHKHKQDPLQPCDTBYPVYQPAIREANGIVECG 1017
 Qy 971 PCQKVFVVOQIPNSNLLLVTDPTCDGSIFFPVVLQATEVKYNASVKCDRMR 1022
 Db 1018 PCQKVFVVOQIPNSNLLLVTDPTCDGSIFFPVVLQATEVKYNASVKCDRMR 1069

RESULT 8
 AAB62261
 ID AAB62261 standard; protein; 1069 AA.
 XX
 AC AAB62261;
 DT 11-JUN-2001 (first entry)
 XX
 Human calcium channel alpha2delta subunit.
 DE
 XX Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;
 KW nervous system disorder; pain; epilepsy; anxiety; human.
 KW
 XX Homo sapiens.
 OS
 XX WO200120336-A2.
 PN
 XX 22-MAR-2001.
 PD
 XX 18-SEP-2000; 2000WO-EP009136.
 PF
 XX 16-SEP-1999; 99US-00397549.
 PR
 XX (WARN) WARNER LAMBERT CO.
 PA
 XX Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;
 PI WPI; 2001-257902/26.
 XX N-PSDB; AAF57569.
 DR
 XX Competitive binding assay for screening ligands which bind a cerebral
 PT cortical voltage-dependent calcium channel alpha2-delta-1 subunit, where
 PT the ligands identified are useful for treating disorders of the nervous
 PT system, including pain.
 XX
 XX Disclosure; Page 151-154; 158pp; English.
 PS
 XX The invention relates to a new method for screening ligands which bind a
 CC cerebral cortical voltage-dependent calcium channel alpha2delta subunit,
 CC preferably alpha2delta-1 subunit. The method comprises contacting a
 CC secreted soluble recombinant alpha2delta-1 subunit with a ligand of
 CC interest and a labelled compound which binds the subunit, followed by
 CC measuring the level of binding of the labelled compound to alpha2delta-1
 CC subunit. The method is useful for screening ligands, preferably
 CC biologically active products that modulate a nervous system function,
 CC which bind a cerebral cortical voltage-dependent calcium channel
 CC alpha2delta-1 subunit. The ligands identified by the method are useful
 CC for treating disorders of the nervous system, including pain, epilepsy
 CC and anxiety. The present sequence represents a human calcium channel
 CC alpha2delta subunit
 XX
 XX Sequence 1069 AA;

Query Match 92.1%; Score 5276; DB 4; Length 1069;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1008; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

RESULT 9
 AAY92324
 ID AAY92324 standard; protein; 1096 AA.
 XX

Qy 11 DRVKLWADTFGGDLNVTNTKYSGSLLLOKQYKDVESLSKIEEVDGLVLRKFSDEMML 70
 Db :
 58 ETVKLWADTFGGDLNVTNTKYSGSLLLOKQYKDVESLSKIEEVDGLVLRKFSDEMML 117
 Qy 71 RRKVEAVQNLVEAABEADLNHEFNESLVFDYNSVLINERDEKGNFVELGABFLLESNAH 130
 Db 118 RRKVEAVQNLVEAABEADLNHEFNESLVFDYNSVLINERDEKGNFVELGABFLLESNAH 177
 Qy 131 FSNLPVNTSISVOLPTNVNKPDPDILNGVYMSSEALNAVVENFORDPTLTWYFGSATG 190
 Db 178 FSNLPVNTSISVOLPTNVNKPDPDILNGVYMSSEALNAVVENFORDPTLTWYFGSATG 237
 Qy 191 FFRYFGIKWTPDENGVIITFDCNRNGWYIOAAATSPKDIVILVDVSGMKGRLMTIAKHTI 250
 Db 238 FFRYFGIKWTPDENGVIITFDCNRNGWYIOAAATSPKDIVILVDVSGMKGRLMTIAKHTI 297
 Qy 251 TTILDTLGENDFVNIITAYNDYVHYIEPCFKGILVQADRDNRHFKLLVBEELMKVGUGVD 310
 Db 298 TTILDTLGENDFVNIITAYNDYVHYIEPCFKGILVQADRDNRHFKLLVBEELMKVGUGVD 357
 Qy 311 QALREAFQILKQFEAKQKSLCNOAATMLISDGAVEDYEPVEKYNMPCDKRVFTYLIIGR 370
 Db 358 QALREAFQILKQFEAKQKSLCNOAATMLISDGAVEDYEPVEKYNMPCDKRVFTYLIIGR 417
 Qy 371 EVSFADRMKWIACNNKGYTQISTLADTQENVMYELHLSRPMVINHDHDIITEAYMDS 430
 Db 418 EVSFADRMKWIACNNKGYTQISTLADTQENVMYELHLSRPMVINHDHDIITEAYMDS 477
 Qy 431 KLLSSQAQSLTLLTTVAMPVFSKNETRSHGILLGVGSDVALRELMLKAPRYKLGWHGY 490
 Db 478 KLLSSQAQSLTLLTTVAMPVFSKNETRSHGILLGVGSDVALRELMLKAPRYKLGWHGY 537
 Qy 491 AFLNTNNGVILSHPDRLPLYREGKLLPKPNYSVDLSEVEDQAESLTAMINRETGT 550
 Db 538 AFLNTNNGVILSHPDRLPLYREGKLLPKPNYSVDLSEVEDQAESLTAMINRETGT 597
 Qy 551 LSMDVKVPMDKGRVILFLTNDYFFTDISDTFSLGAVLSRGHGEYILLGNSTVEEGLHDL 610
 Db 598 LSMDVKVPMDKGRVILFLTNDYFFTDISDTFSLGAVLSRGHGEYILLGNSTVEEGLHDL 657
 Qy 611 LHPDLALAGDWIYCIITDIDPDHRKLSQLEAMIRFLTRKOPDLCEDBELVREVLFDVAVTA 670
 Db 658 LHPDLALAGDWIYCIITDIDPDHRKLSQLEAMIRFLTRKOPDLCEDBELVREVLFDVAVTA 717
 Qy 671 PMEAYWTALALANMSESEHVDMAFLGTRAGLLRSSLFGVSEKVSQRKFLTPDEASVFT 730
 Db 718 PMEAYWTALALANMSESEHVDMAFLGTRAGLLRSSLFGVSEKVSQRKFLTPDEASVFT 777
 Qy 731 LDRFFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAGV 790
 Db 778 LDRFFPLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAGV 837
 Qy 791 QMKLEFLQRFWAATRCSTVDGCTQSCSDSLDCFDVNNNGFILSKSRSTGRFLGE 850
 Db 838 QMKLEFLQRFWAATRCSTVDGCTQSCSDSLDCFDVNNNGFILSKSRSTGRFLGE 897
 Qy 851 VDGAULTQLLSMGVFSQVWYDYQAMCKPSSHHSAAQPLVSPISAFELTATRWLLQELVL 910
 Db 898 VDGAULTQLLSMGVFSQVWYDYQAMCKPSSHHSAAQPLVSPISAFELTATRWLLQELVL 957
 Qy 911 FLEWSVMGWDYRGAEAKSVFHHSHKHKQDPLQPCDTBYPVYQPAIREANGIVECG 970
 Db 958 FLEWSVMGWDYRGAEAKSVFHHSHKHKQDPLQPCDTBYPVYQPAIREANGIVECG 1017
 Qy 971 PCQKVFVVOQIPNSNLLLVTDPTCDGSIFFPVVLQATEVKYNASVKCDRMR 1022
 Db 1018 PCQKVFVVOQIPNSNLLLVTDPTCDGSIFFPVVLQATEVKYNASVKCDRMR 1069

PI	Brown JP, Bertelli F;	
XX	WPI: 2001-235262/24.	
DR	N-PSDB; AAS01431.	
XX	Calcium channel alpha2delta subunits, useful in e.g. SPA assays,	
PT	Flashplate assays, Nickel Flashplate assays, Filter binding assays or	
PT	Wheat Germ Lectin Flashplate assays.	
XX		
PS	Claim 28; Page 149-153; 160pp; English.	
XX		
CC	The present sequence represents human secreted calcium channel	
CC	alpha2delta subunit #16 which is soluble and retains the functional	
CC	characteristics of the full length or wild type alpha2delta subunit	
CC	(AAU01025) from which it is derived. The invention relates to truncated	
CC	alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins	
CC	which retain their affinity for radioactively labelled gabapentin. The	
CC	alpha2delta subunit is 1 of the components of the heteromultimeric	
CC	voltage-dependent calcium channel (VDCC) complexes present in neuronal	
CC	and non-neuronal tissues including heart and skeletal muscle. Numerous	
CC	soluble forms of the human calcium channel alpha2delta subunits (AAU01014	
CC	-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of the porcine	
CC	calcium channel alpha2delta subunits (AAU01027-AAU01031) are described.	
CC	The secreted soluble alpha2delta subunit may be used in assays e.g.	
CC	scintillation proximity assay (SPA), flashplate, nickel flashplate,	
CC	filter binding or wheat germ lectin flashplate assays to detect or	
CC	measure the binding or interaction of a ligand (e.g. gabapentin, L-	
CC	Norleucine, L-Allo-Isoleucine, L-methionine, L-leucine, L-Isoleucine, L-	
CC	valine, Spermine and/or L-Phenylalanine) of a calcium channel alpha2delta	
CC	subunit	
XX		
SQ	Sequence 1050 AA;	

Query Match 90.4%; Score 5179; DB 4; Length 1050;	
Best Local Similarity 99.6%; Pred. No. 0;	
Matches 989; Conservative 1; Mismatches 3; Indels 0; Gaps 0;	
QY	11 DRVKLWADTFGGDLXNTVTYKSGSLLOKKYKDVESLSKTEEVVDGLVLRKPSDEMNMML 70
DB	58 ETVKLWADTFGGDLXNTVTYKSGSLLOKKYKDVESLSKTEEVVDGLVLRKPSDEMNMML 117
QY	71 RRKVEAVQNLEVAEEADLNHEFNESLVPDYNSVLINERDEKGNFVELGAEFLLESNAH 130
DB	118 RRKVEAVQNLEVAEEADLNHEFNESLVPDYNSVLINERDEKGNFVELGAEFLLESNAH 177
QY	131 FSNLPVNTSSSVQLPTNNVYNKDPDILNGVYMSALNAVFNENFQDPDLTWQYFGSATG 190
DB	178 FSNLPVNTSSSVQLPTNNVYNKDPDILNGVYMSALNAVFNENFQDPDLTWQYFGSATG 237
QY	191 FFRIYPGIKWTPDENGVIITDCRNRGWYIOAATSPKDIVILVDVSGMKGLRMTIAKHTI 250
DB	238 FFRIYPGIKWTPDENGVIITDCRNRGWYIOAATSPKDIVILVDVSGMKGLRMTIAKHTI 297
QY	251 TTILDTLGENDFVNIIAYNDYVHYIBPCFKGILVQADRONREHFKLLVEELMVKGVGVD 310
DB	298 TTILDTLGENDFVNIIAYNDYVHYIBPCFKGILVQADRONREHFKLLVEELMVKGVGVD 357
QY	311 QALREAFQILKQFEAKQKSLCNQAIMLISDGAVEDYEPVFEKYNPDCCKVRFTYLIGR 370
DB	358 QALREAFQILKQFEAKQKSLCNQAIMLISDGAVEDYEPVFEKYNPDCCKVRFTYLIGR 417
QY	371 EVSFADRMKWIACNNKGYITQISTLADTQBNVMEYLHLVSRPMVINHDHDIITWEAYMDS 430
DB	418 EVSFADRMKWIACNNKGYITQISTLADTQBNVMEYLHLVSRPMVINHDHDIITWEAYMDS 477
QY	431 KLSSQAQSLTLTTVAMPVFSKKNETRSRGILLGVVGSQDVALRELKMLAPRYKLGVGHY 490
DB	478 KLSSQAQSLTLTTVAMPVFSKKNETRSRGILLGVVGSQDVALRELKMLAPRYKLGVGHY 537
QY	491 AFLNTNNGYILSHPDRLPYREGKLLKPKPNYNSVDLSEVWEDQAESLRTAMINRETGT 550
DB	538 AFLNTNNGYILSHPDRLPYREGKLLKPKPNYNSVDLSEVWEDQAESLRTAMINRETGT 597

QY	551 LMSDVKVPMDKGRVLFNTNDYFFFTDTSIDTPPSLGAVALSRGHGEYILLGNVTSVEEGLHDL 610
DB	598 LMSDVKVPMDKGRVLFNTNDYFFFTDTSIDTPPSLGVVLSRGHGEYILLGNVTSVEEGLHDL 657
QY	611 LHPDLALAGDWIYICITDIDPDHRKLSQLEAMIRFLTRKQPDLECDLBELVREVLFDVAVVTA 670
DB	658 LHPDLALAGDWIYICITDIDPDHRKLSQLEAMIRFLTRKQPDLECDLBELVREVLFDVAVVTA 717
QY	671 PMEAYWTALANMSESEHVDMAFLGTRAGLLRSSLFGVSEKVSQRKFLTPDEASVFT 730
DB	718 PMEAYWTALANMSESEHVDMAFLGTRAGLLRSSLFGVSEKVSQRKFLTPDEASVFT 777
QY	731 LDRFPFLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVMTASTAVAVTVDKRTAIAAAAGV 790
DB	778 LDRFPFLWYRQASEHPAGSFVFNLRWAEGPESAGEPMVMTASTAVAVTVDKRTAIAAAAGV 837
QY	791 QMKLEFLQRFKFWAATRCQSTVDGPTYQSCEDSLDCFCVINDNNGFILLISKRSRRTGRPLGE 850
DB	838 QMKLEFLQRFKFWAATRCQSTVDGPTYQSCEDSLDCFCVINDNNGFILLISKRSRRTGRPLGE 897
QY	851 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHSAAQPLVSPISAFLTATRWLLQELVL 910
DB	898 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHSAAQPLVSPISAFLTATRWLLQELVL 957
QY	911 FFLLEWSVWGSWYDRGAEAKSVFHHSHKHKQDPLOPCDTEYFVYVQPAIREANGIVECG 970
DB	958 FFLLEWSVWGSWYDRGAEAKSVFHHSHKHKQDPLOPCDTEYFVYVQPAIREANGIVECG 1017
QY	971 PCQKVFVWQIQIPNSNLLLVTDPTDCSIFPPV 1003
DB	1018 PCQKVFVWQIQIPNSNLLLVTDPTDCSIFPPV 1050
RESULT 13	
AAB62260	
ID	AAB62260 standard; protein; 1050 AA.
XX	
AC	AAB62260;
XX	
DT	11-JUN-2001 (first entry)
XX	
DE	Human calcium channel alpha2delta subunit.
XX	
KW	Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;
KW	nervous system disorder; pain; epilepsy; anxiety; human.
XX	
OS	Homo sapiens.
XX	
PN	WO200120336-A2.
XX	
PD	22-MAR-2001.
XX	
PF	18-SEP-2000; 2000WO-BP009136.
XX	
PR	16-SEP-1999; 99US-00397549.
XX	
PA	(WARN) WARNER LAMBERT CO.
XX	
PI	Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;
XX	
DR	WPI; 2001-257902/26.
XX	
PT	Competitive binding assay for screening ligands which bind a cerebral
PT	cortical voltage-dependent calcium channel alpha2-delta-1 subunit, where
PT	the ligands identified are useful for treating disorders of the nervous
PT	system, including pain.
XX	
PS	Disclosure; Page 147-150; 158pp; English.
XX	
CC	The invention relates to a new method for screening ligands which bind a
CC	cerebral cortical voltage-dependent calcium channel alpha2delta subunit,
CC	preferably alpha2delta-1 subunit. The method comprises contacting a
CC	secreted soluble recombinant alpha2delta-1 subunit with a ligand of

CC interest and a labelled compound which binds the subunit, followed by
CC measuring the level of binding of the labelled compound to alphadelta-1
CC subunit. The method is useful for screening ligands, preferably
CC biologically active products that modulate a nervous system function,
CC which bind a cerebral cortical voltage-dependent calcium channel
CC alphadelta-1 subunit. The ligands identified by the method are useful
CC for treating disorders of the nervous system, including pain, epilepsy
CC and anxiety. The present sequence represents a human calcium channel
CC alphadelta subunit
XX
SQ Sequence 1050 AA;

Query Match 30.4%; Score 5179; DB 4; Length 1050;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 989; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 DRVQLWADTTGGDLYNTVTYKSGLLQKKYKDVESLKIIEVDGLVRFKSFEDMENML 70
DB :|||||
DB 58 ETVKLWADTTGGDLYNTVTYKSGLLQKKYKDVESLKIIEVDGLVRFKSFEDMENML 117
QY 71 RRKVEAVQNIVEAAEADLNHEFNESLVFDYNSVLINERDEKGNFVELGAELLESNAH 130
DB 118 RRKVEAVQNIVEAAEADLNHEFNESLVFDYNSVLINERDEKGNFVELGAELLESNAH 177
QY 131 FSNLPVNTSSVQLPTNVYKDPDILNGVYMEALNAVFENFQDPTLTWQYFGSATG 190
DB 178 FSNLPVNTSSVQLPTNVYKDPDILNGVYMEALNAVFENFQDPTLTWQYFGSATG 237
QY 191 FFRIYPGIKWTPDENGVIITFCNRGWYIOAATSPKDIVILVDVSGMGLRMTIAKHTI 250
DB 238 FFRIYPGIKWTPDENGVIITFCNRGWYIOAATSPKDIVILVDVSGMGLRMTIAKHTI 297
QY 251 TTILDTLGENDFVNIAYNDVHYIEPCFKGILLVQADRDNRHFKLLVEELVMYKGVGVD 310
DB 298 TTILDTLGENDFVNIAYNDVHYIEPCFKGILLVQADRDNRHFKLLVEELVMYKGVGVD 357
QY 311 QALREAFQILKQAEAKQKGLCNQAIMLSIDGAVEDYEPVEFKYNWPDCKRVFTYLIGR 370
DB 358 QALREAFQILKQAEAKQKGLCNQAIMLSIDGAVEDYEPVEFKYNWPDCKRVFTYLIGR 417
QY 371 EVSFADRMKVIACNKGYYTQISTLADTQENVMYELHVLSPVMVINHDHDIITEAYMDS 430
DB 418 EVSFADRMKVIACNKGYYTQISTLADTQENVMYELHVLSPVMVINHDHDIITEAYMDS 477
QY 431 KLLSSQAQSLTLTTVAMPVFSKNETRSHRGILLGVVGSVDVALRELKMLAPRYKLGVHG 490
DB 478 KLLSSQAQSLTLTTVAMPVFSKNETRSHRGILLGVVGSVDVALRELKMLAPRYKLGVHG 537
QY 491 AFLNTNNGYILSHPDRLPLRYEGKLLKPKPNYNSVDLSEVEDQAESLRTAINRETGT 550
DB 538 AFLNTNNGYILSHPDRLPLRYEGKLLKPKPNYNSVDLSEVEDQAESLRTAINRETGT 597
QY 551 LSMDVKVPMDKGRVLFNTNDYFTDIDSPFSLGAVLSRGHGEYILLGNVTSVEEGLHDL 610
DB 598 LSMDVKVPMDKGRVLFNTNDYFTDIDSPFSLGAVLSRGHGEYILLGNVTSVEEGLHDL 657
QY 611 LHPDLALAGDWIYCIITDIDPDHRLKSLQLEAMIRFLTRKDPDLCEBELVREVLFDVAVTA 670
DB 658 LHPDLALAGDWIYCIITDIDPDHRLKSLQLEAMIRFLTRKDPDLCEBELVREVLFDVAVTA 717
QY 671 PMEAYWTALALNSESSEHVVWDAFLGTRAGLIRRSLSFVSEKVSQRKFLTPDEASVFT 730
DB 718 PMEAYWTALALNSESSEHVVWDAFLGTRAGLIRRSLSFVSEKVSQRKFLTPDEASVFT 777
QY 731 LDRFPLMYROASBHPAGSFVFNLRWAEKPSAGEPMVVTASTAVATVDRKTAIAAAGV 790
DB 778 LDRFPLMYROASBHPAGSFVFNLRWAEKPSAGEPMVVTASTAVATVDRKTAIAAAGV 837
QY 791 QMKLEFLQRKFWAATRCQSTVDGPYQTQSCSDSLDCFDVDDNNGFILLIKSRETGRFLGE 850
DB 838 QMKLEFLQRKFWAATRCQSTVDGPYQTQSCSDSLDCFDVDDNNGFILLIKSRETGRFLGE 897
QY 851 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHSAAQPLVSPISAFLTATRWLLQELVL 910

DB 898 VDGAVLTQLLSMGVFSQVTMYDYQAMCKPSSHHSAAQPLVSPISAFLTATRWLLQELVL 957
QY 911 FULLESVWGSWYDRGAEAASVHFHSHKHKQDPLOPCDTEYPVVYQPAIREANGIVECG 970
DB 958 FULLESVWGSWYDRGAEAASVHFHSHKHKQDPLOPCDTEYPVVYQPAIREANGIVECG 1017
QY 971 PQKQFVWQIQPNSNLLLVTDPTCDCSIFPPV 1003
DB 1018 PQKQFVWQIQPNSNLLLVTDPTCDCSIFPPV 1050

RESULT 14
AA923233
ID AAY92323 standard; protein; 1096 AA.
XX AC AAY92323;
XX DT 10-AUG-2000 (first entry)
XX Human alpha-2-delta-D polypeptide from splice variant 1.
DE alpha-2-delta-D; calcium channel; 12p13.3; gabapentin; cytostatic;
KW anticonvulsant; antimigrane; antiparkinsonian; antidepressant;
KW splice variant.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Misc-difference 310
FT /note= "encoded by RTT"
XX WO200020450-A2.
XX PN 13-APR-2000.
XX PD 07-OCT-1999; 99WO-US023519.
XX PF 07-OCT-1998; 98US-0103322P.
XX PR 30-OCT-1998; 98US-0106473P.
XX PR 29-DEC-1998; 98US-0114088P.
XX PA (WARN) WARNER LAMBERT CO.
XX PI Johns MA, Moldover B, Offord JD;
XX WIPI; 2000-303744/26.
XX DR N-PSDB; AAA09278.
XX New human nucleic acids encoding the alpha2delta-C and alpha2delta-D
XX PT proteins, useful in the treatment of epilepsy, migraine, chronic pain,
XX PT anxiety, multiple sclerosis or cancer.
XX PS Example 3; Page 84; 88pp; English.
XX CC The alpha-2-delta-D gene encodes a calcium channel subunit polypeptide.
CC The gene has been mapped to chromosome 12p13.1. This gene and the related
CC alpha-2-delta-C and -B genes are useful for protecting mammalian cells
CC from abnormal calcium flux by introducing expression vectors containing
CC the respective gene into mammalian cells. The antisense genes are also
CC useful for treating or preventing epilepsy. The alpha-delta-2-A protein
CC is a high-affinity binding target of the anti-convulsant drug gabapentin.
CC Therefore, alpha-delta-2 proteins may also be targeted to treat seizure-
CC related syndromes, migraine, ataxia, vestibular defects, chronic pain,
CC sleep interference, anxiety, amyotrophic lateral sclerosis (ALS), multiple
CC sclerosis, mania, tremor, parkinsonism, substance abuse or addiction
CC syndromes, mood, depression or cancer
XX SQ Sequence 1096 AA;

Query Match 81.2%; Score 4649; DB 3; Length 1096;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 895; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY	11	DRVKLWADTFGGDLVNTVTYKSGSLLLQKKYKDVESLLKIEEVDGLVLRKFSDEMNM	70
Db	58	ETVKLWADTFGGDLVNTVTYKSGSLLLQKKYKDVESLLKIEEVDGLVLRKFSDEMNM	117
QY	71	RRKVEAVQNLVEAAEADLNHEFNESSLVFDYNSVLINERDEKGNFVELGAELLESNAH	130
Db	118	RRKVEAVQNLVEAAEADLNHEFNESSLVFDYNSVLINERDEKGNFVELGAELLESNAH	177
QY	131	FSNLPVNTSSSVQLPNNVYNKDDPDLINGVYMEALNAVFEVFPQDPTLTWQYFGSATG	190
Db	178	FSNLPVNTSSSVQLPNNVYNKDDPDLINGVYMEALNAVFEVFPQDPTLTWQYFGSATG	237
QY	191	FFRIYPGIKWTPBENGVIITFCNRRGWYIOAATSPKDIVILVDVSGMKGRLMTIAKHTI	250
Db	238	FFRIYPGIKWTPBENGVIITFCNRRGWYIOAATSPKDIVILVDVSGMKGRLMTIAKHTI	297
QY	251	TTILDTLGENDFVNIITAYNDVHYIEPCFKGILLVQADRDNRHFKLLVEELVMYKGVGVD	310
Db	298	TTILDTLGENDFXNIIITAYNDVHYIEPCFKGILLVQADRDNRHFKLLVEELVMYKGVGVD	357
QY	311	QALREAFQILKQAEKQSGSLCNOAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR	370
Db	358	QALREAFQILKQAEKQSGSLCNOAIMLISDGAVEDYEPVFEKYNWPDCKVRVFTYLIGR	417
QY	371	EVSFADRMKWIACNNKGYITQISTLADTQENVMYHLVLSRPMVINHDHDIITEAYMDS	430
Db	418	EVSFADRMKWIACNNKGYITQISTLADTQENVMYHLVLSRPMVINHDHDIITEAYMDS	477
QY	431	KLSSQAQSLTLTTVAMPVFSKKNTRSHGILLGVVGSQVALRELMLAPRYKLGVHG	490
Db	478	KLSSQAQSLTLTTVAMPVFSKKNTRSHGILLGVVGSQVALRELMLAPRYKLGVHG	537
QY	491	AFLNTNNGYILSHPDRLPYRECKLKPKNYSVDLSEVEWQDAESLRTAMINRETGT	550
Db	538	AFLNTNNGYILSHPDRLPYRECKLKPKNYSVDLSEVEWQDAESLRTAMINRETGT	597
QY	551	LSMDVKVPMDKGRVFLTNDYFTDIDTPFSLGAVLSRGHGEYILLGNNTSVEEGLHDL	610
Db	598	LSMDVKVPMDKGRVFLTNDYFTDIDTPFSLGAVLSRGHGEYILLGNNTSVEEGLHDL	657
QY	611	LHPDLALAGDWIYCIITIDPDHRLKLSQLEAMITRFLTRKOPDLCEDBELVREVLFDVAVTA	670
Db	658	LHPDLALAGDWIYCIITIDPDHRLKLSQLEAMITRFLTRKOPDLCEDBELVREVLFDVAVTA	717
QY	671	PMEAYWTALANNSESEHVVDMAFILGTRAGLRSILFVSGSEKVSQRKFLTPEDEASVFT	730
Db	718	PMEAYWTALANNSESEHVVDMAFILGTRAGLRSILFVSGSEKVSQRKFLTPEDEASVFT	777
QY	731	LDRFPLWYRQASRHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAGV	790
Db	778	LDRFPLWYRQASRHPAGSFVFNLRWAEGPESAGEPMVVTASTAVAVTVDKRTAIAAAGV	837
QY	791	QMKLEFLQRFKWAATRCQCTVDPGYTQSCEDSDLDCEFDVNNNGFILLIKSRRETGRFLGE	850
Db	838	QMKLEFLQRFKWAATRCQCTVDPGYTQSCEDSDLDCEFDVNNNGFILLIKSRRETGRFLGE	897
QY	851	VDGAVLTQLLSMGVFSQVTMYDQAMKPSHHSSAAQPLVSPISAFLTATRWLLQELVL	910
Db	898	VDGAVLTQLLSMGVFSQVTMYDQAMKPSHHSSAAQPLVSPISAFLTATRWLLQELVL	957

RESULT 15
AAE13285

ID AAE13285 standard; protein; 1310 AA.

XX AAE13285;

XX AAE13285;

DT 12-FEB-2002 (first entry)

XX Human transporters and ion channels (TRICH)-12.

XX Human; transporter and ion channel; TrICH; akinesia; cystic fibrosis;

diabetes mellitus; Parkinson's disease; myasthenia gravis; dementia; cardiac disorder; angina; hypertension; myocarditis; hyperglycaemia; neurological disorder; Alzheimer's disease; cataract; infertility; Wilson's disease; schizophrenia; Grave's disease; Addison's disease; Huntington's disease; multiple sclerosis; meningitis; hypotensive; cardiant; nootropic; neuroprotective; neuroleptic; ophthalmological; antithyroid; anticonvulsant; goitre; antiinflammatory.

Homo sapiens.

WO200177174-A2.

18-OCT-2001.

06-APR-2001; 2001WO-US011206.

06-APR-2000; 2000US-0195595P.

12-APR-2000; 2000US-0196872P.

20-APR-2000; 2000US-0199020P.

28-APR-2000; 2000US-0200552P.

05-MAY-2000; 2000US-020348P.

11-MAY-2000; 2000US-0203495P.

(INCY-) INCYTE GENOMICS INC.

Reddy R, Thornton M, Borowsky ML, Tang YT, Khan FA, Tribouley CW; Gandhi AR, Yao MG, Sanjanwala MS, Baughn MR, Nguyen DB, Policky JL; Yue H, Sellhammer JJ, Wallia NK, Lal P, Kearney L, Walsh RT, Lu DAM; Lu Y, Greene BD, Raumann BE, Patterson C;

WPI; 2002-017448/02.

N-PSDB; AAD22004.

Polypeptides of human transporters and ion channels, useful for diagnosing, treating or preventing disorders of transport, neurological, muscle, immunological and cell proliferative disorders.

Claim 1; Page 132-135; 150pp; English.

The invention relates to human transporters and ion channels (TRICH) and the polynucleotides encoding them. The composition comprising TRICH or agonist of TRICH is useful for treating a disease or condition associated with decreased expression of functional TRICH or condition associated with overexpression of TRICH respectively. The composition comprising Ab is useful for diagnosing a condition of disease associated with expression of TRICH in a subject, where the disorders include a transport disorder such as akinesia, cystic fibrosis, diabetes mellitus, Parkinson's disease, myasthenia gravis, cardiac disorders associated with transport e.g. angina, hypertension, myocarditis, neurological disorders associated with transport e.g. Alzheimer's disease, Wilson's disease, schizophrenia, cataracts, infertility, hyperglycaemia, Grave's disease, goitre, Addison's disease, Huntington's disease, dementia, multiple sclerosis, bacterial and viral meningitis. TRICH DNA is useful for generating a transcript image of a tissue or cell type, which represents the global pattern of gene expression by a particular tissue or cell type and for analysing the proteome of a tissue or cell type. TRICH DNA is used in gene therapy. The present amino acid sequence is human TRICH12 protein

Sequence 1310 AA;

Query Match 66.5%; Score 3808; DB 5; Length 1310;
Best Local Similarity 80.5%; Pred. No. 0;
Matches 750; Conservative 4; Mismatches 14; Indels 164; Gaps 2;

QY 11 DRVKLWADTFGGDLVNTVTYKSGSLLLQKKYKDVESLLKIEEVDGLVLRKFSDEMNM 70

Db 374 ETVKLWADTFGGDLVNTVTYKSGSLLLQKKYKDVESLLKIEEVDGLVLRKFSDEMNM 433

QY 71 REKVEAVQNLVEAAEADLNHEFNESSLV----- 98

Db 434 RRKVEAVQNLVEAAEADLNHEFNESSLVPGVGVGVMSTQSGVGVGMSVTQSGVGV 493

Qy	99	-----	98
Db	494	GVGMSITLSGVGVGMSVRQSGVGVGMSVTQSGVGVGMSVTQSGVGVGMSVRQ	553
Qy	99	-----	98
Db	554	SGVGVGMSVTQSGVGVGMSVRQSGVGVGMSVTQSGVGVGMSVTQSGVGVGMSVRQ	613
Qy	99	-----	98
Db	614	SVGLTRPPQFDYNSVLINERDEKGNFVLCAGFLLSENAHFNLPVNTSISSVQLPTNV	673
Qy	150	YNKDPDILNGVYNSVLCAGFLLSENAHFNLPVNTSISSVQLPTNV	209
Db	674	YNKDPDILNGVYNSVLCAGFLLSENAHFNLPVNTSISSVQLPTNV	733
Qy	210	FDCKNRGMYIQATSPKDIIVLVDVSGMGLRMTIAKHITTTITLDTLGENDFWIIAYN	269
Db	734	FDCKNRGMYIQATSPKDIIVLVDVSGMGLRMTIAKHITTTITLDTLGENDFWIIAYN	793
Qy	270	DYVHYIEPCFKGILVQADNRNREHFLLVEELMVKGVGVDQALREAFQILKQFQEAQKQ	329
Db	794	DYVHYIEPCFKGILVQADNRNREHFLLVEELMVKGVGVDQALREAFQILKQFQEAQKQ	853
Qy	330	SLCNOAILMSDGAVEDYEPVEFKYNWPCDKVRVFTYLI GREVSFADRMKWIACNNKGY	389
Db	854	SLCNOAILMSDGAVEDYEPVEFKYNWPCDKVRVFTYLI GREVSFADRMKWIACNNKGY	913
Qy	390	TQSTLADTQENWYELHVLSPMPVINHDHDIITWEAYMDSKLLSSOQSLTLLTTVAMP	449
Db	914	TQSTLADTQENWYELHVLSPMPVINHDHDIITWEAYMDSKLLSSOQSLTLLTTVAMP	973
Qy	450	VFSKKNETRSHGILLGVVGSVALRELMLAPRYKLGVGHYAFLNTNNGYILSHPDRLPL	509
Db	974	VFSKKNETRSHGILLGVVGSVALRELMLAPRYKLGVGHYAFLNTNNGYILSHPDRLPL	1033
Qy	510	YREGKKLKPKNYNSVDLSEVEDQAESLRTAMINRETGTLSMDVKVPMDKGRVLFIT	569
Db	1034	YREGKKLKPKNYNSVDLSEVEDQAESLRTAMINRETGTLSMDVKVPMDKGRVLFIT	1093
Qy	570	NDYFFTDISTPFSGLGAVLSRGHGEYILGNTSVEEGLHDLHPDLALAGDWIYCIITDID	629
Db	1094	NDYFFTDISTPFSGLGAVLSRGHGEYILGNTSVEEGLHDLHPDLALAGDWIYCIITDID	1153
Qy	630	PDRKLSQLEAMIRFLTRKDPDLECDSEELVREVLFDVAVTAPMEAYWTALANMSESEH	689
Db	1154	PDRKLSQLEAMIRFLTRKDPDLECDSEELVREVLFDVAVTAPMEAYWTALANMSESEH	1213
Qy	690	VDMAPLGTAGLRLSSLFVSGSEKVSQRKFLTPEDEASVFTLDRFPLWYQASEHPAGSF	749
Db	1214	VDMAPLGTAGLRLSSLFVSGSEKVSQRKFLTPEDEASVFTLDRFPLWYQASEHPAGSF	1273
Qy	750	VFNLRWAEGPESAGEPMTASTAVATVDKR	781
Db	1274	VFNLRWAEGPESAGEPMTASTAVATVDKR	1302

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